

Figure 1

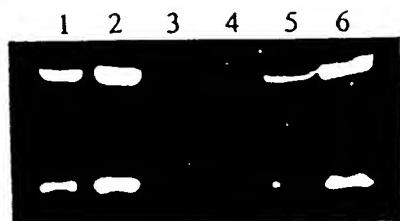


Figure 2

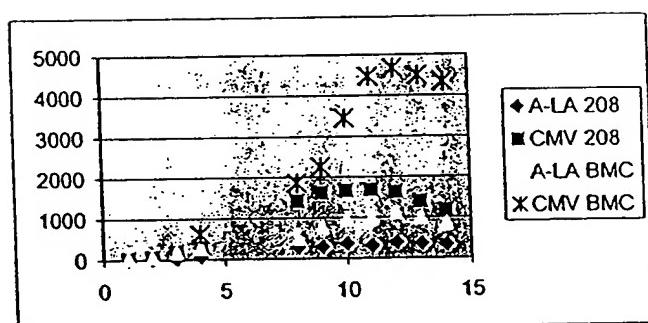
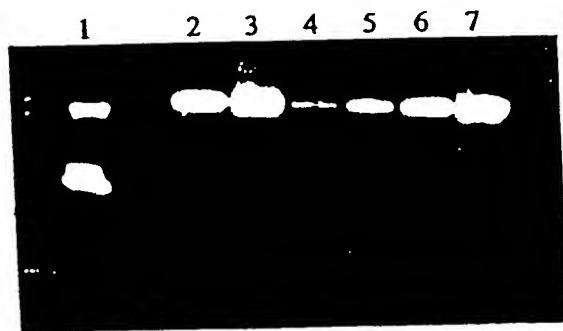


Figure 3



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Figure 4
SEQ ID NO:1
Hybrid Human-Bovine Alpha-Lactalbumin Promoter

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1      GATCAGTCCTGGTGGTCAATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51     AATACTTTGGCCACCTGATGCGAAGAAGTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
101    ATACTGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151    GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201    AGGAGTTGGTAATGGGAGGGAGGCTGGCGTGTGCACTCCATGGGGTT
251    GCAAAGAGTTGGCAACTTGAGTGACTGAAGTCAACTGATAGTGTAAATC
301    CATGGTACAGAATATAGGATAAAAAGAGGAAGAGTTGCCCCGATTTCTG
351    AAGAGTTGTTAGGATATAAAAGTTAGAATACCTTTAGTTGGAAGTCTTA
401    ATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451    AGAGACTGATGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501    ATTGGTTATAGCTGTTACAATATATAACCAATATATAACCAATATATTGGTTATATA
551    GCATGAAGCTTGATGCCAGCAATTGAGGAACCCATTAGAAGCTAGTATC
601    CTAACACTCATGTTCCAGGACACTGATCTTAAGGTCAGGTTCAAGAT
651    CTGTTTATAGGCTCTAGGTGTATATTGTTGGGGTCTGGGCTTGGCTCA
701    GATGGTAAAGTGTCTGCCATGTGGGTGATCTGGGTTGATCCCCTGG
751    CTTGGGAAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801    ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAAGCTACAGTCCATGGG
851    ATTGCAAAGAGGTTGAACACAACGTGAGCAACTAAGCACAGCACAGTACAGT
900    ATACACCTGTGAGGTGAAGTGAAGTCAATGCAGGGTCTCCTGC
951    ATTGCAGAAAGATTCTTACCATCTGAGCCACCAAGGGAAAGCCAAGAATA
1001   CTGGAGTGGGTAGCCTATTCTCTCCAGGGGATCTTCCCCTCCAGGAA
1051   TTGAACTGGAGTCTCTGCATTTCAGGTGGATTCTCACCAAGCTGAACTA
1101   CCAGCTGGATACTACTCCAAATATTAAAGTGTAAAGTCCAGTTTCCCA
1151   CCTTCCCCAAAGGGTGGTCACTCTTTTAACCTTCTGTGGCCTACT
1201   CTGAGGCTGCTACAAGCTTATATATTATGAACACATTTATTGCAAGTT
1251   GTTAGTTTAGATTACAATGTGGTATCTGGCTATTAGTGGTATTGGTG
1301   GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351   ATACACACTTTCAAGTCTCCATTGGTGAATAGAAAGTCTCTGGAT
1401   CTAAGTTATATGTGATTCTCAGTCTGTGGTCATATTCTATTCTACTCC
1451   TGACCACTCAACAAGGAACAGATATCAAGGGACACTTGTGGTTCA
1501   TGCGCTGGGTGGAGTGGGGCATGACATATGTTGGGCTTGTACATGGC
1551   TGGATTGGTGGACAAGTGCCAGCTGTGATCCTGGGACTGTGGCATGTGA
1601   TGACATACACCCCTCTCCACATTCTGCATGTCCTAGGGGGAAAGGGGG
1651   AAGCTCGGTATAGAACCTTATTGTATTCTGATTGCCCTACTCTTAT
1701   ATTGCCCCCATGCCCTCTTGTCTCAAGTAACCAAGAGACAGTGCCTC
1751   CCAGAACCAACCCACAAGAAACAAAGGGCTAAACAAAGCCAAATGGAA
1801   GCAGGATCATGGTTGAACTCTTCTGGCCAGAGAACAAACATCTGCTATG
1851   GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901   AGCTGGCAGGCTCAGCTTCTGTCTGGCATGCCAGTCTCTCTCATT
1951   CTCTTCTAGATGTAGGGCTTGGTACCAAGAGCCCTGAGGGTTCTGCAT
2001   GAATATAAAATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTGGGG
2051   GCGCGAATTGAGCTCGGTACCCGGGATCTCGAGGGGGCCCGGTAC
2101   C

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- 1 - 1525 Bovine alpha lactalbumin 5' flanking region (-2000 to -550 from the bovine alpha-lactalbumin transcription start point)
- 1526 - 2056 Human alpha-lactalbumin 5' flanking region (-600 to +15 from the human alpha-lactalbumin transcription start point)
- 2057 - 2101 Multiple cloning site

Figure 5
SEQ ID NO:2
Mutated PPE Sequence

1 GATTACTTACTGGCAGGTGCTGGGGCTTCCGAGACAATCGCGAACATCT
51 ACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGACGCG
101 GCGGTGGTAATTACAAGCGAGGATCCGATTACTTACTGGCAGGTGCTGGG
151 GGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTCGACC
201 AGGGTGAGATATCGGCCGGGACGCGGGTGGTAATTACAAGCG

1 - 119 Mutated PPE
120 -126 Linker
127 - 245 Mutated PPE

Figure 6
SEQ ID NO:3
IRES-Signal Peptide Sequence

1 GGAATTGCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCGAAGCCG
51 CTTGGAAATAAGGCCGGTGTGCGTTGTCTATATGTTATTTCAACCATAT
101 TGCGTCTTTGGCAATGTGAGGGCCGGAAACCTGGCCCTGTCTTCTG
151 ACGAGCATTCCCTAGGGCTTTCCTCTGCCAAAGGAATGCAAGGTCT
201 GTTGAATGTCGTGAAGGAAGCAGTTCTCTGGAAGCTTCTTGAAGACAAA
251 CAACGTCTGTAGCGACCCCTTGCAAGGCAGCGGAACCCCCCACCTGGCGAC
301 AGGTGCCTCTGCCGCCAAAGCCACGTGTATAAGATAACACCTGCAAAGGC
351 GGCACAAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTC
401 AATGGCTCTCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCAGAAAG
451 GTACCCCATTGTATGGGATCTGATCTGGGCTCGGTGCACATGCTTTAC
501 ATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCGAACACGGGG
551 ACGTGGTTCTCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGGCGCCATGG
601 TCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGGCGCCATGG
651 GATATCTAGATCTCGAGCTCGCGAAAGCTT

1 - 583 IRES
584 - 640 Modified bovine alpha-lactalbumin signal peptide coding region
641 - 680 Multiple cloning site

Figure 7a
SEQ ID NO:4
CMV MN14 Vector

1 CCGATCCGCCATTAGCCATTATTACGGTTATAGCATAATCAA
51 TATTGGCTATTGGCATTGCATACGTTGTATCCATATCATAATATGTACA
101 TTTATATTGGCTCATGTCACATTACGCCATTGGTACATTAGTCAGCCCATA
151 ACTAGTTATTAAATAGTAATCAATTACGGGCTATTAGTCAGCCCATA
201 TATGGAGTCCCGCTTACATAACTTACGGTAAATGGCCCGCTGGCTGAC
251 CGCCAACGACCCCCGCCCCATTGACGTCATAATAGACGTATGTTCCATA
301 GTAGCCTAATAGGACTTCCATTGACGTCATAATGGGTGGAGTATTTACG
351 GTAAACTGCCCACTTGGCAAGTACATCAAGTGATCATATGCCAGTACGC
401 CCCCTATTGACGTCATGACGGTAAATGGCCCGCTGGCATTATGCCAG
451 TACATGACCTTATGGGACTTCTACTTGGCAGTACATCTACGTATTAGT
501 CATCGCTATTACCATGGTATGCGGTTTGGCAGTACATCAATGGCGTG
551 GATAGCGGTTGACTCACGGGATTTCCAAGTCTCCACCCATTGACGTC
601 AATGGGAGTTGTTGGCACC AAAATCAACGGGACTTCCAAAATGTCG
651 TAACAACCTCCGGGCCCCATTGACGCAAAATGGGCGGTAGGCATGTACGGTGG
701 AGGTCTATATAAGCAGAGCTGTTAGTGAACCGTCAGATGCCCTGGAGA
751 CGCCATCCACCGCTGTTTGACCTCCATAGAAGACACCGGGACCGATCCAG
801 CCTCCGGGCCCCAAGCTCTCGACGGATCCCCGGGATTAGGACCTCA
851 CCATGGGATGGAGCTGTATCATCCTCTTCTGGTAGCAACAGCTACAGGT
901 GTCCACTCCGAGGTCCAACCTGGTGGAGAGCGGTGGAGGTGTGCAACC
951 TGGCCGGTCCCTGCGCTGTCCCTGCTCCGCATCTGGCTTCGATTTCACCA
1001 CATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAAGGTCTTGAGTGG
1051 ATTGGAGAAAATTCTACAGATAGCAGTACGATTAACTATGCCGTCTCT
1101 AAAGGATAGATTTACAATATCGCGAGAACACGCCAGAACACATTGTTCC
1151 TGCAAATGGACAGCCTGAGACCCGAAGACACCGGGCTATTGGTGCA
1201 AGCCTTACTTCGGCTCCCCCTGGTTGCTTATTGGGGCCAAGGGACCC
1251 GGTCACCGTCCTCCTCAGCCTCCACCAAGGGCCATGGCTTCCGGCTGG
1301 CACCCCTCTCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGCTGCC
1351 GTCAGGACTACTCCCCAACCGGTGACGGTGGAAACTCAGCAGC
1401 CCTGACCAGCGCGTGACACCTTCCGGTGTCTCAGTCCAGCAGCTGG
1451 TCTACTCCCTCAGCGTGGTGACCGTGGCTCCAGCAGCTGGCACC
1501 CAGACCTACATCTGCAACGTGAATCAAGGCCAGCAACACCAAGGTGG
1551 CAAGAGAGTTGAGCCAAATCTTGTGACAAGAACATCACACATGCC
1601 GCCCAGCACCTGAACCTCTGGGGGACCGTCAGTCTCCTCTCCCCCA
1651 AAACCCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTACATGCG
1701 GGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACG
1751 TGACGGCGTGGAGGTGATAATGCCAAGAACAGCCGGGGAGGAGCAG
1801 TACAACAGCACCGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACCA
1851 CTGGCTGAATGGCAAGGAGTACAAGTGCAGGTCTCAACAAAGCCCTCC
1901 CAGCCCCCATCGAGAAAACCATCTCAAAGCCAAGGGCAGCCCGAGAA
1951 CCACAGGTGACACCCCTGCCCCATCCGGGAGGAGATGACCAAGAACCA
2001 GGTCAAGCTGACCTGCTGGTCAAAGGCTTCTATCCCAGCGACATGCC
2051 TGGAGTGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCC
2101 CCCGTGCTGGACTCCGACGGCTCTTCTCTATAGCAAGCTCACCGT
2151 GGACAAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCC
2201 ACAGGGCTCTGCACAACCAACTACACGCAAGAGGCCTCTCC
2251 GGGAAATGAAAGCGAATTGCCCTCTCCCTCCCCCCCCCTAACGT
2301 CTGGCGGAAGCCGTTGGAATAAGGCCGGTGTGCGTTGTATATGTTA
2351 TTTCCACCATATTGCCGTCTTGGCAATGTGAGGGCCGGAAACCTGG
2401 CCTGCTCTCTGACGAGCATTCTAGGGCTTTCCTCTGCCAAAG
2451 GAATGCAAGGTCTGTGAATGTCGTGAAGGAAGCAGTCTCTGGAAAGCT
2501 TCTTGAAGAACACCGTCTGTAGCGACCCCTTGCAGGCAGCGAACCC
2551 CCCACCTGGCGACAGGTGCCTCTGCCCAAAAGCCACGTATAAGATA
2601 CACCTGCAAAGCGGCACAACCCCAAGTGCACCTGTGAGGTGGATAGTT
2651 GTGGAAAGAGTCAAATGGCTCTCTCAAGCGTATTCAACAAAGGGCTGAA
2701 GGATGCCAGAAGTACCCATTGATGGGATCTGATCTGGGCCCTCG
2751 GCACATGCTTACATGTGTTAGTCGAGGTAAAAAAACGTCTAGGCCCC
2801 CGAACCAACGGGACGTGGTTCTTGTGAAACACGATGATAATATGG

Figure 7b

2851 CCTCCTTGTCTCTGCTCTGGTAGGCATCCTATTCCATGCCACCCAG
2901 GCCGACATCCACGCTGACCCAGAGCCAAAGCAGCCTGAGCGCCAGCGTGGG
2951 TGACAGAGTGACCATCACCTGTAAGGGCCAGTCAGGATGTGGGTACTTCTG
3001 TAGCCTGGTACCCAGCAGAAGCCAGGTAAAGGCTCCAAAGCTGCTGATCTAC
3051 TGGACATCCCACCCGGCACACTGGTGCCAAGCAGATTCAAGCGGTAGCGG
3101 TAGCGGTACCGACTTCACCTCACCATCAGCAGCCTCAGGCCAGAGGACA
3151 TCGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTGTTCTGGCCAA
3201 GGGACCAAGGTGGAATCAAACGAACGTGGCTGCACCATCTGTTCT
3251 CTTCCGCCATCTGATGAGCAGTTGAAATCTGGAACGTGCTCTGTTGT
3301 GCCTGCTGAATAACTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTG
3351 GATAACGCCCTCCAATCGGTAACTCCAGGAGAGTGTACAGAGCAGGA
3401 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAG
3451 CAGACTACGAGAAAACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGC
3501 CTGAGCTGCCCGTCAAAAGAGCTTCAACAGGGAGAGTGTAGAGATC
3551 TAGGCCTCTAGGTCGACATCGATAAAAATAAAAGATTTATTAGTCTCC
3601 AGAAAAAGGGGGAAATGAAAGACCCCACCTGTAGGTTGGCAAGCTAGCT
3651 TAAGTAACGCCATTGCAAGGCATGAAAAATACATAACTGAGAATAGA
3701 GAAGTTCAAGATCAAGGTCAAGGAACAGATGGAACAGCTGAATATGGGCCAA
3751 ACAGGGATATCTGTTGAGCAGTTCTGCCCGCTCAGGGCCAAGAACAA
3801 GATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTTGAGCAGTT
3851 CTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCCGCTCAGCC
3901 CTCAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGCCCCAAGGAC
3951 CTGAAATGACCCCTGTGCCATTATTGAACTAACCAATCAGTTGCTTCTCG
4001 CTTCTGTTGCCGCGCTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAAAC
4051 CCCTCACTCGGGCGCCAGTCCTCCGATTGACTGAGTCGCCGGGTACCC
4101 GTGTATCCAATAAAACCTCTTGCAAGTTGCATCCGACTTGTGGTCTCGCTG
4151 TTCCCTGGGAGGGTCTCTGAGTGATTGACTACCCGTAGCGGGGGTC
4201 TTTCATT

- 1 - 812 CMV promoter/enhancer
853-855 MN14 antibody heavy chain gene signal peptide start codon
2257 - 2259 MN14 antibody heavy chain gene start codon
2271 - 2846 EMCV IRES
2847 - 2849 Bovine alpha-lactalbumin signal peptide start codon
2904 - 2906 First codon mature MN14 antibody light chain gene
3543 - 3544 MN14 antibody light chain gene stop codon
3614 - 4207 MoMuLV 3' LTR

Figure 8a
SEQ ID NO:5
CMV LL2 Vector

1 GGATCCGGCATTAGCCATTATTACGGTTATAGCATAAATCAAT
51 ATTGGCTATTGGCATTGACATCGTTGATCCATATCATAATATGTACAT
101 TTATATTGGCTCATGTCAAACATTACGCCATGGACATTGATTATTGA
151 CTAGTTATTAAATAGTAATCAATTACGGGGCATTAGTCATAGCCATAT
201 ATGGAGTTCCCGTACATAACTTACCGTAATGGCCGCTGGCTGACC
251 GCCCAACGCCACCCGCCATTGACGTCATAATGACGTATGTCATAGCCATAT
301 TAACGCCAATAGGGACTTCCATTGACGTCATAATGACGTATGTCATAGCCATAG
351 TAAACTGCCACTTGGCAGTACATCAAGTGATCATATGCCAAGTACGCC
401 CCCATTGACGTCATAATGACGGTAATGGCCGCTGGCATTATGCCAGT
451 ACATGACCTTATGGGACTTCCATTGACGTCAGTACATCTACGTATTAGTC
501 ATCGCTATTACCATGGTGTGCGGTTTGGCAGTACATCAATGGCGTGG
551 ATAGCGGTTTACTCACGGGATTTCAAGTCTCACCCATTGACGTC
601 ATGGGAGTTTGTGACCAAAATCAACGGGACTTCCAAAATGTCGT
651 AACAACTCCGCCATTGACGCAAATGGCGTAGGCATGTCAGGTGGGA
701 GGTCTATATAAGCAGAGCTGTTAGTGAACCGTCAGATCGCCTGGAGAC
751 GCCATCCACGCTGTTTGACCTCCATAGAAGACACCGGACCGATCCAGC
801 CTCCCGGCCAACGCTCTGACGGATCCCCGGAATTAGGACCTCAC
851 CATGGGATGGAGCTGATCATCCTCTTGTAGCAACAGCTACAGGTG
901 TCCACTCCCAGGTCAGCTGGTCCAATCAGGGCTGAAGTCAGAACCT
951 GGGTCATCAGTGAAGGTCTCTGCAAGGCTTCTGGCTACACCTTACTAG
1001 CTAUTGGCTGCACTGGGTCAGGCAGGCACCTGGACAGGGCTGGAAATGGA
1051 TTGGATACATACTCTAGGAATGATTACTGAGTACAATCAGAACTTC
1101 AAGGACAAGGCAACATACTGACGAGCAATCCACCAATACAGCCTACAT
1151 GGAGCTGAGCAGCTGAGGTCTGAGGACACGGCATTTTATTTGTGCAA
1201 GAAGGGATATTACTACGTTCTACTGGGGCAAGGCACACGGTCACCGTC
1251 TCCTCAGCCTCACCAAGGGCCATGGTCTCCCCCTGGCACCCCTCCTC
1301 CAAGAGCACCTCTGGGGCACAGGCCCTGGCTGCCTGGTAAGGACT
1351 ACTTCCCGAACCGTGACGGTGTCTGGAAACTCAGGCGCCCTGACCCAGC
1401 GGCCTGCACACCTTCCCGTGTCTACAGTCCTCAGGACTCTACTCCCT
1451 CAGCAGCTGGTACCGTCCAGCAGCTGGGACCCAGACCTACA
1501 TCTGCAACGTAATCACAAGCCCAGAACACCAAGGTGGACAGAGATT
1551 GAGCCAAATTTGTGACAAAATCACACATGCCAACCGTCCCCAGCACC
1601 TGAACCTCTGGGGGACCGTCAGTCCTCTTCCCCAAAACCCAAGG
1651 ACACCCCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGAC
1701 GTGAGCCAGGAAGACCTGAGGTCAAGTCAACTGGTACGTGGACGGGT
1751 GGAGGTGATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAACAGCA
1801 CGTACCGTGTGGTCAGCTCCCTCACCGTCTGCCACCCAGGACTGGCTGAAT
1851 GGCAGGGAGTACAAGTGCAGGTCTCCAAACAGCCCTCCAGGCGG
1901 GGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCCACAGGTGT
1951 ACACCCCTGCCCTATCCGGGAGGAGATGACCAAGAACCCAGGTGAGCTG
2001 ACCTGCCCTGGTCAAAGGTTCTATCCCAGCGACATGCCGTGGAGTGGGA
2051 GAGCAATGGCAGCCGAGAACAAACTACAAGACCAAGCCTCCGTGTGG
2101 ACTCCGACGGCTCTTCTCTATAGCAAGCTACCGTGGACAAGAGC
2151 AGGTGGCAGGGAAACGTCTTCTCATGCTCGTGTGACAGGAGCTCT
2201 GCACAAACCATACACGAGAACAGGCTCTCCCTGTCTCCCCGGAAATGAA
2251 AGCCGAATTGCCCTCTCCCTCCCCCCCCCTAACGTTACTGCCGAAG
2301 CCGCTGGATAAGGCCGTGCGTTGTCTATGTTATTTCCACCA
2351 TATTGCCGTCTTGGCAATGTGAGGGCCGAAACCTGGCCCTGTCTC
2401 TTGACGAGCATTCTAGGGGTCTTCCCTCTGCCAAAGGAATGCAAGG
2451 TCTGTTGAATGTCGTGAAGGAAGCAGTCTCTGGAGCTCTGAAGAC
2501 AAACAAACGTCGTAGGCCACCCCTTGCAGGCAGCGAACCCCCCACCTGGC
2551 GACAGGTGCCCTCTGCCGCCCCAACGGCACGTGATAAGATAACCTGCAA
2601 GGCAGCACAACCCAGGCCACGTGTCAGTGTGAGTTGGATAGTTGTGGAAAGAG
2651 TCAAATGGCTCTCTCAAGCGTATCAACAAGGGCTGAAGGATGCCAG
2701 AAGGTACCCATTGTATGGGATCTGATCTGGGCCCTCGTGCACATGCTT
2751 TACATGTGTTAGTCGAGGTTAAAAAAACGTCTAGGCCCGAACACAG
2801 GGGACGTGGTTTCTTGTGAAACACGATGATAATGCCCTTGT

Figure 8b

2851 CTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGACATCC
2901 AGCTGACCCAGTCTCCATCATCTCTGAGCGCATCTGGAGATAGGTG
2951 ACTATGAGCTGTAAGTCCAGTCAGTCAAAGTGTATACAGTGAAATCACAA
3001 GAACTACTGGGCTGGTACCGAGAAACCAGGGAAAGCACCCTAAACTGC
3051 TGATCTACTGGCATCCACTAGGGAACTCTGGTGTCCCTCGCGATTCT
3101 GGCAGCGGATCTGGGACAGATTTACTTCACCACATCAGCTCTTCAACC
3151 AGAACAGACATTGCAACATATTATTGTCACCAATACCTCTCGTGGACGT
3201 TCGGTGGAGGGACCAAGGTGCAAGATCAAACGAACGTGTTGACCATCT
3251 GTCTTCATCTCCCGCATCTGATGAGCAGTTGAAATCTGGAACGTGCTC
3301 TGTTGTGTGCTGTAACTTCTATCCCAGAGAGGCAAAGTACAGT
3351 GGAAGGTGGATAACGCCCTCAATCGGTAACTCCAGGAGAGTGTACA
3401 GAGCAGGACAGAAGGACAGCACCTACGCCCTCAGCAGCACCTGACGCT
3451 GAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGAAGTCACCC
3501 ATCAGGGCTGAGCTGCCGTACAAGAGCTTCAACAGGGAGAGTGT
3551 TAGAGATCTAGGCCCTCTAGGTCGACATCGATAAAAATAAAAGATTTATT
3601 TAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCACCTGTAGGTTGGCA
3651 AGCTAGCTTAAGTAACGCCATTGCAAGGCATGGAAAAATACATAACTG
3701 AGAATAGAGAAGTTCAGATCAAGGTCAAGGTCAGGAACAGATGGAACAGCTGAATA
3751 TGGGCCAAACAGGATATCTGGTAAGCAGTTCTGCCCGGCTCAGGGC
3801 CAAGAACAGATGGAACAGCTGAATATGGCCAACAGGATATCTGTGGTA
3851 AGCAGTTCTGCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCC
3901 GTCCAGCCCTCAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGCC
3951 CCAAGGACCTGAAATGACCCCTGTGCCATTGGAACTAACCAATCAGTTC
4001 GCTTCTCGCTTCTGTTCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAG
4051 CCCACAACCCCTCACTCGGGCGCCAGTCCTCCGATTGACTGAGTCGCC
4101 GGGTACCCGTGTATCCAATAAACCTCTTGCAGTTGCATCCGACTTGTGG
4151 TCTCGCTTCTGGGAGGGTCTCCTCTGAGTGAATGACTACCCGTCA
4201 GTCTTCATT

1 - 812	CMV promoter/enhancer
852 - 854	LL2 antibody heavy chain signal peptide start codon
2247 - 2249	LL2 antibody heavy chain stop codon
2261 - 2836	EMCV IRES
2837 - 2839	Bovine alpha-lactalbumin signal peptide start codon
2894-2896	First codon of mature LL2 antibody light chain gene
3551 - 3553	LL2 antibody light chain gene stop codon
3622 - 4210	MoMuLV 3' LTR

Figure 9a
SEQ ID NO:6
MMTV MN14 Vector

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1      CGAGCTTGGCAGAAATGGTGAACCTCCGAGAGTGTCCTACACCTAGGGG
51     AGAAGCAGCCAAGGGTTGTTCCACCAAGGACGACCCGTCGCGCAC
101    AACGGATGAGCCCATTAGACAAAGACATATTCATCTCTGCTGCAAACCTT
151    GGATAGCTCTGCTTGCCTGGCTATTGGGGAAAGTTGCAGGTCGTGC
201    TCGCAGGGCTCTCACCCTGACTCTTCAATAAAACTCTCTGCAAG
251    ATTACAATTAACAAATTGGAGAACTCGACCTCCTGAGGCAAGGA
301    CCACAGCCAACCTCCCTTACAAGCCGATCGATTTGTCCTCAGAAAT
351    AGAAAATAAGAATGCTTGCTAAAATTATTTTACCAATAAGACCAATC
401    CAATAGGTAGATTATTAGTTACTATGTTAGAAATGAATCATTTATCTTT
451    AGTACTATTTTACTCAAATTCAAAGTTAGAAATGGGAATAGAAAATAG
501    AAAGAGACGCTCAACCTCAATTGAAGAACAGGTCAAGGACTATTGACCA
551    CAGGCCTAGAAGTAAAAAGGGAAAAAAAGAGTGTGTCAGGAAATAGGA
601    GACAGGTGGTGGCAACCCAGGGACTTATAGGGGACCTACATCTACAGACC
651    AACAGATGCCCTTACCATATAACAGGAAGATATGACTTAAATTGGGATA
701    GGTGGTTACAGTCATGGCTATAAGTGTATATAGATCCCTCCCTTT
751    CGTAAAAGACTCGCCAGAGCTAGACCTCCTGGTGTATGTTGTCAGAAG
801    AAAGAAAAGACGACATGAAACAACAGGTACATGATTATTTATCTAGGAA
851    CAGGAATGCACTTTGGGAAAGATTTCACCAAGGAGGGGACAGTG
901    GCTGGACTAATAGAACATTCTGCAAAAACCTATGGCATGAGTTATT
951    TGATTAGCCTGATTGCCAACCTTGCCTTCCAAAGGCTTAAGTAAGT
1001   TTGGTTACAAACTGTTCTTAAACAAAGGATGTGAGACAAGTGGTTCC
1051   TGACTTGGTTGGTATCAAAGGTTCTGATCTGAGCTCTGAGTGTCTATT
1101   TTCTATGTTCTTGGAAATTATCAAATCTTATGTAATGCTTATGTA
1151   AACCAAGATATAAAAGAGTGTGATTGGAGTAAACCTTGCACAGTC
1201   TAACATTCACCTTGTGTTGTGCTGTTGCCATCCCGTCTCGC
1251   CGTCACTTATCCTTCACTTCCAGAGGGTCCCCCGCAGACCCGGCGAC
1301   CCTCAGGTGGCGACTGGCGAGCTGGCGCCCCAACAGGGACCCCTCGGA
1351   TAAGTAGCCCTGCTTATTCTACTATTTGTTGTTGTCCTGTTG
1401   CTCTATCTGTGCTGGCTATCATACAAGAGCGGAACGGACTCACCTCAGG
1451   GAACCAAGCTAGCCGGGTGACCGATCCGATTACTACTGGCAGGTGC
1501   TGGGGCTCCGAGACAATCGGAACATCTACACCACACAACACCGCCTC
1551   GACCAGGGTAGAGATATCGGCCGGGACGCCGGTGGTAATTACAAGCGA
1601   GATCCGATTACTACTGGCAGGTGCTGGGGCTCCGAGACAATCGCGAA
1651   CATCTACACCCACAAACGCCCTCGACCAGGGTAGATATCGGCCGGGG
1701   ACGGGGGGTGGATTACAAGCGAGATCCCCGGAAATTCAAGGACCTCAC
1751   CATGGATGGAGCTGTATCATCCTCTTCTGGTAGCAACAGCTACAGGTG
1801   TCCACTCGGGTCCAACCTGGGGAGCGGTGGAGGGTGTGTCACCT
1851   GGCCTGGTCCCTGCGCTGTCTGCCTGCATCTGGCTTCGATTTCAACAC
1901   ATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGA
1951   TTGGAGAAATTATCCAGATAGCAGTACGATTAACTATGCCGCTCTA
2001   AAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCT
2051   GCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTGTC
2101   GCCTTTACTCGGCTCCCTGGTTGCTTATTGGGGCAAGGGACCCCG
2151   GTCACCGTCTCCTCAGCCTCACCACAGGGCCCATGGCTTCCCCCTGGC
2201   ACCCTCCTCCAAGAGCACCTCTGGGGCACAGGGCCCTGGCTGCCTGG
2251   TCAAGGACTACTTCCCGAACCGGTGACGGTGTGTCGTGAACTCAGGC
2301   CTGACCAGGGCGTGCACACCTTCCCGTGTCTACAGTCCCTCAGGACT
2351   CTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTGGCACC
2401   AGACCTACATCTGCAACGTGAATACAAGCCCAGCAACACCAAGGTGGAC
2451   AAGAGAGTTGAGCCAAATCTTGTGACAAAACCTACACATGCCACCGTG
2501   CCCAGCACCTGAACTCTGGGGGACCGTCAGTCTCTTCTTCCCCCAA
2551   AACCCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTACATGCGTG
2601   GTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGT
2651   GGACGGCGTGGAGGTGATAATGCAAGACAAGCCGGGGAGGAGCAGT
2701   ACAACAGCACGTACCGTGTGGTCAGCGTCTCACCGTCTGCACCAAGGAC
2751   TGGCTGAATGGCAAGGAGTACAAGTGCAGGTTCTCAAACAAAGCCCTCCC
2801   AGCCCCCATCGAGAAAACCATCTCCAAAGCCAAGGGCAGCCCCGAGAAC

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Figure 9b

2851 CACAGGTGTACACCTGCCCCATCCGGGAGGAGATGACCAAGAACAG
2901 GTCAGCCTGACCTGCCTGGTCAAAGGTTCTATCCCAGCGACATGCCGT
2951 GGAGTGGAGAGCAATGGCAGCCGAGAACAACTACAAGACCACGCCCTC
3001 CGTGCTGGACTCGACGGCTCCTCTCTCTATAGCAAGCTCACCGTG
3051 GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTATGCTCCGTGATGCA
3101 CGAGGCTCTGACAACCACACTACACGAGAAGAGCTCTCCCTGCTCCCG
3151 GGAATGAAAGCGAATTGCCCTCTCCCTCCCCCCCCCTAACGTTAC
3201 TGGCCGAAGCCGCTTGGAAATAAGGCCGGTGTGCCTTGTCTATATGTTAT
3251 TTCCACCATATTGCCCTTGGCAATGTGAGGGCCGGAAACCTGGC
3301 CCTGCTCTTGTACGAGCATTCCTAGGGTCTTCCCTCTGCCAAAGG
3351 AATGCAAGGCTGTTGAATGTCGTAGCGACCCCTTCAGGCAGCGAACCCC
3401 CCACCTGGCAGGGTGCCTCTGGCCAAAAGCCACGTGTATAAGATAC
3451 ACCTGCAAAGCGGCACAACCCAGTGCACGTGTGAGTTGGATAGTTG
3501 TGAAAAGAGTCAAATGGCTCTCCTCAACGCTATTCAACAAGGGGCTGAAG
3551 GATGCCAGAGTACCCATTGTATGGATCTGATCTGGGCTCGGTG
3601 CACATGTTTACATGTGTTAGTCGAGGTTAAAAAAACGTCAGGCCCC
3651 CGAACACGGGAGCTGGTTTCTTGTGAAAAACACGATGATAATATGGC
3701 CTCCCTTGTCTCTGCTCTGGTAGGCATCCTATTCCATGCCACCCAGG
3751 CCGACATCCAGCTGACCCAGAGCCAAGCAGCTGAGCGCCAGCGTGGGT
3801 GACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTCTGT
3851 AGCCTGGTACAGCAGAACGCCAGTAAGGCTCAAAGCTGCTGATCTACT
3901 GGACATCCACCCGGCACACTGGTGTGCAAGCAGATTCAAGGGTAGCGGT
3951 AGCGTACCGACTTCACCTCACCATCAGCAGCTCCAGCCAGAGGACAT
4001 CGCCACCTACTACTGCGCAATATGCCCTATCGGTCTGTTGGGCAAG
4051 GGACCAAGGTTGAAATCAAACGAACTGTGGCTGACCCTGTCATC
4101 TTCCCGCCATCTGATGAGCAGTTGAATCTGGAACTGCCCTGTGTTGTG
4151 CCTGCTGAATAACTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGG
4201 ATAACGCCCTCAATGGGTAACTCCCAGGAGAGTGTACAGAGCAGGAC
4251 AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGC
4301 AGACTACGAGAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCC
4351 TGGCTCGGGCTCAAAAGAGCTTCAACAGGGAGGTGTTAGAGATCC
4401 CCCGGGCTGAGGAATTGATATCAAGCTTATCGATAATCAACCTCTGGA
4451 TTACAAAATTGTGAAAGATTGACTGGTATTCTTAACATATGTTGCTCCTT
4501 TTACGCTATGTGGATACGCTGCTTAAATGCCCTGTATCATGCTATTGCT
4551 TCCCGTATGGCTTCATTTCTCTCTGTATAAAATCTGGTTGCTGTC
4601 TCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCA
4651 CTGTGTTGCTGACGCAACCCACTGGTGGGCATTGCCACCCACTGT
4701 CAGCTCCTTCCGGGACTTCGCTTCCCTCCCTATTGCCACGGCGGA
4751 ACTCATGCCGCCCTGCCCTGGCCCTGCTGGACAGGGCTCGCTGTTGG
4801 GCACTGACAATTCCGTGGTGTGTCGGGAAATCATGCTCTTCTTGG
4851 CTGCTCGCTGTGTTGCCACCTGGATTCTGCCGGGACGTCCTCTGCTA
4901 CGTCCCTCGGCCCTCAATCCAGGGACCTTCCCTCCGCCCTGCTGC
4951 CGGCTCTGGCCCTCTCCGCTTCCGCTTCGCCCTCAGACGAGTCGG
5001 ATCTCCCTTGGGCCGCTCCCCGCTGATGATAACCGTCAACATGATA
5051 AAATAAAAGATTTATTAGTCCTCAGAAAAAGGGGAAATGAAAGACCC
5101 CACCTGAGGTTGGCAAGCTAGCTTAAGCTAACGCCATTGCAAGGGCAT
5151 GAAAAAAATACATAACTGAGAAATAGAGAAGTTCAAGATCAAGGTCAAGGAACA
5201 GATGGAACAGCTGAATATGGCCAAACAGGATATCTGTTGAAAGCAGTT
5251 CTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAA
5301 ACAGGATATCTGTTGTAAGCAGTCTGCCCGCTCAGGGCCAAGAAC
5351 GATGGTCCCCAGATGCGGTCCAGGCCCTCAGCAGTTCTAGAGAACCATCA
5401 GATGTTCCAGGGTGCCTCAAGGACCTGAAATGACCCCTGTCGCTTATTG
5451 AACTAACCAATCAGTTCGCTTCTCGCTTGTGCGCGCTTCTGCTCCC
5501 CGAGCTCAATAAAAGGCCACAACCCCTCACTCGGGGCCAGTCCTCC
5551 GATTGACTGAGTCGCCGGTACCGTGTATCCAATAACCCCTTGCAG
5601 TTGCATCCGACTTGTGGTCTCGCTTGTCTGGGAGGGTCTCCTCTGAGT
5651 GATTGACTACCCGTCAGCGGGGGTCTTCATT
5701

Figure 9c

1752 - 1754	MN14 heavy chain signal peptide start codon
3156 - 3158	MN14 heavy chain stop codon
3170 - 3745	EMCV IRES
3746 - 3748	Bovine alpha-lactalbumin signal peptide start codon
3803 - 3805	First codon of mature MN14 light chain gene
4442 - 4444	MN14 antibody light chain gene stop codon
4487 - 5078	WPRE sequence
5133 - 5372	MoMuLV 3' LTR

Figure 10a
SEQ ID NO:7
Alpha-Lactalbumin MN14 Vector

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1      AAAGACCCCAACCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTGC
51     AGGCATGGAAAAATACATAACTGAGAATAGAAAAGTCAGATCAAGGTCA
101    GGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGAAGCGGTT
151    CCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATGGGCC
201    AACACAGGATATCTGTGGAAGCAGTCCCTGCCCGGCTCGGGGCAAGAA
251    CAGATGGTCCCAGATGCGGCCAGCAGCTTCTAGTGAATCAT
301    CAGATGTTCCAGGGTCCCCAAGGACCTGAAAATGACCCTGTACCTTAT
351    TTGAACTAACCAATCAGTCGCTTCTCGCTTCTGTTCGCGCGCTCCGCT
401    CTCCGAGCTCAATAAAAGAGGCCAACCCCTCACTCGGCGGCCAGTCT
451    TCCGATAGACTGCGTCGCCCGTACCCGTTCCCAATAAGCCTCTTG
501    CTGTTGCATCGAATCGGGTCTCGCTGTTCTGGGAGGGTCTCCCT
551    GAGTGAATTGACTACCCACGACGGGGTCTTCATTGGGGGCTGTCGGG
601    GATTGGAGACCCCTGCCAGGGACCCGACCCACCACCGGAGGTAAG
651    CTGGCCAGCAACTTATCTGTCTGTCCGATTGCTAGTGTCTATGTTG
701    ATGTTATGCGCCTGCGTGTACTAGTTAGCTAAGTAGCTCTGTATCTGG
751    CGGACCCGTGGTGAACCTGACGAGTTCTGAACACCCGGCCAACCCCTGG
801    GAGACGTCCCAGGGACTTGGGGCGCTTTGTGGCCCGACCTGAGGAA
851    GGGAGTCGATGTGAATCCGACCCCGTCAAGGATATGTGGTTCTGGTAGGA
901    GACGAGAACCTAAACAGTCCCCGCTCCCGTCTGAATTGGCTTCTGGT
951    TTGGAACCGAAGCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTT
1001   TGTTGTCCTGCTGACTGTGTTCTGTATTGCTGAAATTAGGGC
1051   CAGACTGTTACCACTCCCTTAAGTTGACCTTAGGTCACTGGAAAGATGT
1101   CGAGCGGATCGCTACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGG
1151   TTACCTCTGCTCTGCAGAAATGGCCACCTTTAACGTCGGATGGCCGCGA
1201   GACGGCACCTTAACCGAGACCTCATCACCCAGGTTAACATCAAGGTCTT
1251   TTCACCTGGCCCGATGGACACCCAGACCAGGTCCTACATCGTGACCT
1301   GGGAAAGCCTGGCTTTGACCCCCCTCCCTGGGTCAGGCCCTTGTACAC
1351   CCTAAGCCTCCGCTCTTCCATCCGCCGCTCTCCCCCTTGA
1401   ACCTCCTCGTTCGACCCCGCTCGATCCTCCCTTATCCAGCCCTCACTC
1451   CTTCCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAGGATC
1501   GTTTCGCATATTGAACAAAGATGGATTGACCGCAGGTTCTCCGGCCGCTT
1551   GGGTGGAGGGTATTGGCTATGACTGGGACAAACAGACAATCGGCTGC
1601   TCTGATGCCCGCTGTTCCGGCTGTCAGCGCACGGGGCCGGTTCTTTT
1651   TGTCAGACCGACCTGTCGGTGCCTGAATGAACACTGCAGGACGAGGCAG
1701   CGCGGCTATCGTGGCTGCCACGACGGCGTCCCTGCGCAGCTGTGCTC
1751   GACGTTGTCACTGAAGCGGGAAAGGGACTGGCTGCTATTGGCGAAGTGCC
1801   GGGGCAGGATCTCTGTATCTCACCTGCTCTGCCGAGAAAGTATCCA
1851   TCATGGCTGATGCAATGCCGGCTGCATACGTTGATCCGGTACCTGC
1901   CCATTGACCAACAGCAGAACATCGCATCGAGCGAGCAGTACTCGGAT
1951   GGAAGCGGGTCTTGTGATCAGGATGATCTGGACGAAGGACATCAGGGGC
2001   TCGCGCCAGCGAACCTGGCTGCCAGGCTCAAGGCCGCGATGCCGACGGC
2051   GAGGATCTCGTGTGACCCATGGCGATGCCCTGTTGCCGATATCATGGT
2101   GGAAAATGGCGCTTTCTGGATTCTGACTGTGGCGGCTGGGTGTGG
2151   CGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAG
2201   CTTGGCGGCGAATGGGTGACCGCTTCTCGTGTCTTACGGTATGCCGC
2251   TCCCGATTCGCAGCGCATCGCCTCTATGCCCTCTGACCGATTCTTCT
2301   GAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAACCTGC
2351   CATCACCGAGATTCTGATTCCACCGCCCTCTATGAAAGGGTTGGGCTTC
2401   GGAATCGTTTCCGGGACGCCGGCTGGATGATCTCCAGCGCGGGGATCT
2451   CATGCTGGAGTTCTCGCCCACCCGGGCTCGATCCCTCGCGAGTTGGT
2501   TCAGCTGCTGCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
2551   AAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCCATGC
2601   CCCCGAACTGCAAGGAGTGGGGAGGCACGATGCCGTTGGTCGAGGGGG
2651   ATCCTAGAACTAGCGAAAATGCAAGAGCAGGAAACATGCCACACA
2701   TGAGGAATACCGATTCTCTCATTAACATATTGAGGCAAGTATCTGGGCT
2751   TAAAGCAGAAGTCCAACCCAGATAACGATCATATACATGGTTCTCCA
2801   GAGGTTCATTAAGTGAACACTCGTCCGAGAATAACGAGTGGATCAGTCTG

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Figure 10b

2851 GGTGGTCATTGAAAGGACTGATGCTGAAGTGAAGCTCCAATACTTGGC
2901 CACCTGATGCCAAGAACTGACTCATGTGATAAGACCCCTGATACTGGGAAA
2951 GATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAAGAGTTGGATGG
3001 AATCACCAACTCGATGGACATGAGTTGAGCAAGCTTCAGGAGTTGGTA
3051 ATGGGCAGGGAAAGCCTGGCGTGCAGTCCATGGGTTGCAAAGAGTTG
3101 GACACTACTGAGTGAUTGAACCTGAACGTGATAGTGTAACTCCATGGTACAGA
3151 ATATAGGATAAAAAAGAGGAAGAGTTGCCCTGATTCTGAAGAGTTGTAG
3201 GATATAAAAGTTAGAATACCTTAGTTAGTTGAAAGTCTAAATTATTTACT
3251 TAGGATGGTACCCACTGCAATATAAGAAATCAGGCTTAGAGACTGATG
3301 TAGAGAGAATGAGCCCTGGCATAACCGAACGCTAACAGCTATTGGTTATAG
3351 CTGTTATAACCAATATAACCAATATTGGTTATATAGCATGAAGCTT
3401 GATGCCAGCAATTGAGAAGCATTAGAACTAGTATCCTAAACTCTAC
3451 ATGTTCCAGGACACTGATCTAAAGCTCAGGTCAGAATCTGTTTATA
3501 GGCTCTAGGTGTATATTGTTGGGCTTCCCTGGTGGCTCAGATGGTAAAGT
3551 GTCTGCCTGCAATGTGGGTGATCTGGGTTGATCCCTGGCTTGGGAAAGAT
3601 CCCCTGGAGAAGGAAATGCCAACCCACTCTAGTACTCTTACCTGGAAAAT
3651 TCCATGGACAGAGGAGGAGCTTGTAAAGCTACAGTCATGGGATGCAAAGAG
3701 TTGAACACAACGTGAGCAACTAACGACAGCACAGTACAGTATACACCTGTG
3751 AGGTGAAGTGAAGTGAAGGTTCAATGCAAGGGTCTCCTGCATTGAGAAAAG
3801 ATTCTTACCATCTGAGCCACCAGGAAAGGCCAAGAAACTTGGAGTGGGT
3851 AGCCTATTCCCTCTCAGGGATCTCCCATCCAGGAATTGAACTGGAG
3901 TCTCTGCATTTCAGGTGGATTCTCACCAAGCTGAACCTACCAAGGGATA
3951 CTACTCCAATATAAAGTGTAAAGTCCAGTTTCCCACCTTCCCCAAA
4001 AAGGTTGGGTCACTTTTAAACCTTCTGTCGGCTACTCTGAGGCTGTC
4051 TACAAGCTTATATATTTATGAAACACATTATTGCAAGTTGTTAGTTTAG
4101 ATTACAAATGTGGTATCTGGCTATTAGTGGTATTGGTGGTGGGATGG
4151 GGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTCATACACACTT
4201 TCAAGTTCTCATTGGTCAATTAGAAAGTCTCTGGATCTAAGTTATAT
4251 GTGATTCTCAGTCTCTGTTGTCATATTCTATTCTACTCCTGACCACTCAA
4301 CAAGGAACCAAGATATCAAGGGACACTGTTTGTTCATGCCCTGGTTG
4351 AGTGGGCCATGACATATGTTCTGGGCTTGTACATGGCTGGATTGGTTG
4401 GACAAGTGCCAGCTGATCCTGGGACTGTGGCATGTGATGACATACACC
4451 CCCTCTCCACATTCTGCATGTCCTAGGGGGAAAGGGGGAAAGCTCGTAT
4501 AGAACCTTTATTGTATTCTGATTGCCCTACTCTTATATTGCCCTCAT
4551 GCCCTTCTTGTCTCAAGTAACAGAGACAGTGTCTCCAGAACCAAC
4601 CCTACAAGAACAAAGGCTAAACAAAGCCAATGGGAAGCAGGATCATG
4651 GTTGAACTCTTCTGGCCAGAGAACAAACACTGCTATGGACTAGATACT
4701 GGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGAAGCTGGCAGGC
4751 TCAGCGTTCTGCTTGCATGACCAGTCTCTCTTCAATTCTCTTCTAGA
4801 TTAGGGCTTGGTACCAAGAGGCCCTGAGGTTCTGTCATGAATATAAATA
4851 TATGAAACTGAGTGTGCTTCCATTCAAGGTCTTGGGCGCCGAATTCT
4901 GAGCTCGGTACCGGGGATCTCGACGGATCCGATTACTACTGGCAGGTG
4951 CTGGGGCTTCCGAGACAATCGCAACATCTACACCAACACCGCT
5001 CGACCAAGGTGAGATATCGCCGGGAGCGCGCGGTGTAATTACAAGCG
5051 AGATCCGATTACTACTGGCAGGTGCTGGGGCTTCCGAGACAATCGCGA
5101 ACATCTACACCAACACCGCCTGACCGACGGTGAGATATCGGCCGGG
5151 GACCGCGCGGTGTAATTACAAGCGAGATCCCCGGAAATTAGGACCTCA
5201 CCATGGGATGGAGCTGATCATCCTCTTGTGAGCAACAGCTACAGGT
5251 GTCCACTCCGAGGTCCAACACTGGTGGAGAGCGGTGGAGGTGTGCAACC
5301 TGCCCGGTCCCTGCGCTGTCCCTGTCGACATCTGGCTTCAATTTCACCA
5351 CATATTGGATGAGTTGGTGGAGACAGGCACCTGAAAAGGTCTTGAGTGG
5401 ATTGGAGAAATTCAACAGATAGCAGTACGATTAACCTATGCCCTCTCT
5451 AAAGGATAGATTCAACATATCGCGAGACAACGCCAAGAACACATTGTTCC
5501 TGCAAATGGACAGCCTGAGACCCGAAGACACCGGGGCTATTGGGGCCAAGGGACCCC
5551 AGCCTTTACTTGGCTTCCCTGGTTGCTATTGGGGCCAAGGGACCCC
5601 GGTCAACCGTCTCCTCACGCCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
5651 CACCCCTCTCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGCTGCCCTG
5701 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGTTGAACTCAGGCC
5751 CCTGACCAGCGCGTGCACACCTTCCCGCTGTCCTACAGTCCTCAGGAC
5801 TCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGACC
5851 CAGACCTACATCTGCAACGTGAATACAAGCCAGCAACACCAAGGTGGA
5901 CAAGAGAGTTGAGCCAAATCTGTGACAAAACTCACACATGCCACCGT

Figure 10c

5951 GCCCAGCACCTGAACTCCGGGGGACCGTCAGTCTTCCCTTCCCCCA
6001 AAACCCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTACATGCCT
6051 GGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTAGC
6101 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGGAGGAGCAG
6151 TACACAGCACGTACCGTGTGGTCAGCGTCCCTACCCTGCACCAGGA
6201 CTGGCTGAATGCCAAGGAGTACAAGTCAAGGTCTCCAACAAAGCCCTCC
6251 CAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAA
6301 CCACAGGTGTACACCCCTGCCCATCCGGGAGGAGATGCCAACGAAACCA
6351 GGTCAAGCTGACCTGCTGGTCAAAGGCTTCTATCCCAGCGACATGCCG
6401 TGGAGTGGGAGGCCAATGGGAGGCCAGAACACTAACAGAACACGCC
6451 CCCGTGCTGGACTCCGACGGCTCTTCTTCTCTATAGCAAGCTCACCGT
6501 GGACAAGGAGCAGGTGGCAGGGGAACGTCTTCTATGCCGTGATGC
6551 ACGAGGCTCTGCACAACCAACTACACGCCAGAACAGGCCCTCCCTGCTCCC
6601 GGGAAATGAAAGCCGAATTGCCCTCTCCCTCCCCCCCCCTAACGTTA
6651 CTGGCCGAAGCCGCTTGGATAAGGCCGGTGTGCGTTGTCTATATGTTA
6701 TTTCCACCATATTGCCGTCTTGGCAATGTGAGGGCCCGAAACCTGG
6751 CCTCTGCTCTTGACGAGCATTCTAGGGGCTTCCCTCTCGCCAAAG
6801 GAATGCAAGGTCTGTGAATGTGTGAAGGAACAGTCTCTTGAAAGCT
6851 TCTGAAAGACAACACCGTGTAGGCCACCCCTTGAGGCCAGGGAAACCC
6901 CCCACCTGGCAGGGCATTCTGGCAGGCCAAAGCCACGTGTATAAGATA
6951 CACCTGCAAAGGCGGCACAACCCCAGTGCCACGTGTGAGTTGGATAGTT
7001 GTGAAAGACTCAAATGGCTCTCTCAAGCGTATTCAACAAGGGCTGAA
7051 GGATGCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGCTCGGT
7101 GCACATGCTTACATGTGTTAGTCAGGTTAAAAAAACGCTTAGGCCCC
7151 CGGAACACGGGAGCTGTTTCTTGGAAAAAACACGATGATAATATGG
7201 CCTCTTGTCTCTGCTCTGGTAGGCATCCTATTCCATGCCACCCAG
7251 GCCGACATCCAGTCACCCAGAGGCCAACAGCAGCTGAGGCCAGCGTGG
7301 TGACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGTACTTCTG
7351 TAGCCTGGTACCAAGCAGAACGGCTCAAAGCTGCTGATCTAC
7401 TGGACATCCACCCGGCACACTGGTGTGCCAACGAGATTCAAGCGTAGCG
7451 TAGCGGTACCGACTTCACCTCACCATCAGCAGCCTCCAGCCAGAGGACA
7501 TCGCCACCTACTACTGCCAGCAATATAGCCTATCGGTGTTGGCCAA
7551 GGGACCAAGGTGAAATCAAACGAACGGCTGCAACCATCTGCTTCT
7601 CCTCCCGCCATCTGATGAGCTGGTAAATCTGAAACTGCCCTGTTGTG
7651 GCTCTGCTGATAACTCTATCCCAGAGGGCCAAGTACAGTGGAAAGGTG
7701 GATAACGCCCTCCAATGGGTAACTCCCAAGGAGGTGTACAGAGCAGGA
7751 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAG
7801 CAGACTACGAGAAACACAAAGTCTACGCCCTGCCAACGTCACCCATCAGGG
7851 CTGAGCTGCCGTCAACAGAGCTCAACAGGGGAGAGTGTAGAGATC
7901 CCCCGGGCTGAGGAATTGATATCAAGCTTATCGATAATCAACCTCTGG
7951 ATTACAAAATTGTGAAAGATTGACTGGTATTCTTAAACTATGTTGCTCT
8001 TTACGCTATGTTGATGCCCTTAAATGCCCTTGTATCATGCTATTGC
8051 TTCCCGTATGGCTTCTATTTCTCTCTGTGTTGATTAATCTGGTTGCTGT
8101 CTCTTATGAGGAGTTGTTGGCCCGTTGTCAGGCCACGTGGCTGGTGTG
8151 ACTGTGTTGCTGACGCCACCCCACTGGTGGGCAATTGCCACCCACTG
8201 TCAGCTCTTCCGGACTTCGCTTCCCCCTCCCTATTGCCACGGCGG
8251 AACATCGCCGCTGCTTGGCCCGTGTGGACAGGGCTCGCTGTTG
8301 GGCACATGACAATTGGCTGGTGTGTCAGGGAAATCATGTCCTTCTCTG
8351 GCTGCTGCCGTGTTGCCACCTGGATTCTGCCGGGACGCTCTGCTG
8401 ACGTCCCTCGGCCCTCAATCCAGGGACCTTCTCCGCCCTGCTG
8451 CCGGCTCTGCCCTTCCGCCGCTTCAGGCCCTGACGAGTCG
8501 GATCTCCCTGGGCCCTCCCCCTGATCGATACCGTCAACATCGAT
8551 AAAATAAAAGATTATTTAGTCTCCAGAAAAGGGGGAAATGAAAGACC
8601 CCACCTGTAGGTTGGCAAGCTAGCTTAAGTAACGCCATTGCAAGGCA
8651 TGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAAGGAAC
8701 AGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTTGAAAGCAGTT
8751 CCTGCCCGGCTCAGGGCAAGAACAGATGGAACAGCTGAATATGGGCA
8801 AACAGGATATCTGTTGTAAGCAGTCTCTGCCCGGCTCAGGGCAAGAAC
8851 AGATGGTCCCAGATGCCGTCAGGCCCTCAGCAGTTCTAGAGAACCATC
8901 AGATGTTCCAGGGTGCCCAAGGACCTGAAATGACCCCTGTCCTTATT
8951 GAACTAACCAATCAGTCGCTTCGCTCTGTCGCGCTCTGCTCC
9001 CCGAGCTCAATAAGAGGCCACAACCCCTACTCGGGGCCAGTCCTC

Figure 10d

9051 CGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCTCTTGCA
9101 GTTGCATCCGACTTGTGGTCTCGCTGTTCTGGGAGGGTCTCCTCTGAG
9151 TGATTGACTACCCGTCAGCGGGGGTCTTCATT

1 - 658	MoMuSV 5' LTR
659 - 1468	Extended packaging region
1512 - 2306	Neomycin resistance gene
2661 - 4896	Bovine/human alpha-lactalbumin 5' flanking region
5084 - 5327	Double mutated PPE sequence
6207 - 6209	MN14 antibody heavy chain gene signal peptide start codon
6611-6613	MN14 antibody heavy chain stop codon
6625 - 7200	EMCV IRES
7201 - 7203	Bovine alpha-lactalbumin signal peptide start codon
7258 - 7260	First codon of mature MN14 antibody light chain gene
7897 - 7899	MN14 antibody light gene stop codon
7938 - 8529	WPRE sequence
8600 - 9138	Moloney murine leukemia virus 3' LTR

Figure 11a
SEQ ID NO:8
Alpha-Lactalbumin Bot Vector

1 GATCAGTCCTGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51 AATACTTGGCCACCTGATGCGAAGAACGTGACTCATGTGATAAGACCTG
101 ATACTGGAAAGATTGAAGGCAGGGAGAAGGGATGACAGAGGATGGAA
151 GAGTTGGATGGAATCACCACACTCGATGGACATGAGTTGAGCAAGCTTC
201 AGGAGTTGGTAATGGGCAGGGAAAGCTGGCGTGCTGCAGTCATGGGTT
251 GCAAAGAGTTGGACACTACTGAGTGACTGAACTGATAGTGTAACTC
301 CATGGTACAGAATATAGGATAAAAAGAGGAAGAGTTGCCCTGATTCTG
351 AAGAGTTGTAAGGATATAAAAGTTAGAATACCTTAGTTGGAAGTCTTA
401 AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTT
451 AGAGACTGATGAGAGAAATGAGCCCTGGCATACCAGAACGTAACAGCT
501 ATTGGTTATAGCTGTTATAACCAATATATAACCAATATTGGTTATATA
551 GCATGAAGCTGATGCCAGCAATTGAAGGAACCATTTAGAAACTAGTATC
601 CTAAACTCTACATGTTCCAGGACACTGATCTAAAGCTCAGGTTCAGAAT
651 CTTGTTTATAGGCTCTAGGTGATATTGTGGGGCTTCCCTGGTGGCTCA
701 GATGGTAAAGTGTGCTGCAATGTGGGTGATCTGGGTTGATCCCTGG
751 CTTGGGAAAGATCCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801 ACCTGGAAAATTCCATGGACAGGGAGCTGTAAAGCTACAGTCCATGGG
851 ATTGCAAAGAGGTTGAACACAACGCAACTGAGCAACTAACGACAGTCAGT
901 ATACACCTGTGAGGTGAAGTGAAAGGTTCAATGCAGGGCTCCTGC
951 ATTGCAGAAAGATTCTTACCATCTGAGCCACCAAGGGAAAGCCAAGAATA
1001 CTGGAGTGGGTAGCCCTATCCCTCCAGGGATCTTCCCACCCAGGAA
1051 TTGAACTGGAGTCTCCTGCATTCAGGTGGATTCTCACCAAGCTGAACTA
1101 CCAGGTGGATACTACTCCAATATTAAAGTGTAAAGTCCAGTTTCCA
1151 CCTTCCCAAAAAGGTTGGGCACTCTTTTAACCTCTGTGGCTACT
1201 CTGAGGGCTGCTCAAGCTTATATTTATGAAACACATTATTGCAAGTT
1251 GTTAGTTTATGATTTACAATGTGGTATCTGGTATTAGTGGTATTGGTG
1301 GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351 ATACACACTTTCAAGTTCTCCATTGGTGAAGGAAAGTCTCTGGAT
1401 CTAAGTTATATGTGATTCTCAGTCTGTGGTCAATTCTATTCTACTCC
1451 TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTGTTGTTCA
1501 TGGCTGGGTGAGTGGGCATGACATATGTTCTGGGCTTGTACATGGC
1551 TGGATTGGTGGACAAGTGGCAGCTGTGATCTGGACTGTGGCATGTGA
1601 TGACATACACCCCTCTCCACATTCTGCATGTCTAGGGGGAAAGGGGG
1651 AAAGCTGGTATAGAACCTTATTGTATTCTGATTGCTCACTTCTTAT
1701 ATTGCCCTCATGCCCTTTTGTCTCAAGTAACCAAGAGACAGTGCTTC
1751 CCAGAACCAACCTACAAGAAACAAAGGGCTAAACAAAGCCAATGGGAA
1801 GCAGGATCATGGTTGAACCTTTCTGGCCAGAGAACAAACACGCTATG
1851 GACTAGATACTGGGAGAGGGAAAGGAAAGTAGGGTGAATTATGGAAGGA
1901 AGCTGGCAGGCTCAGCGTTCTGCTTGGCATGACCGAGTCTCTCTTCATT
1951 CTCTTCTAGATGTAGGGCTTGGTACCGAGGCCCCCTGAGGCTTCTGCA
2001 GAATATAATATGAAACTGAGTGTGATGCTTCATTTCAGGTTCTGGGG
2051 GCGCGAATTGAGCTGGTACCCGGGATCTGACGGATCCGATTACTT
2101 ACTGGCAGGTGCTGGGGCTTCCGAGACAATCGCGAACATCTACACCA
2151 CAACACCGCCTCGACCAGGGTGGAGATATCGGCCGGGACGGGGCGGTGG
2201 AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGGCTTCCG
2251 GACAATCGCGAACATCTACACCAACACACCGCCTCGACCCAGGGTGAGA
2301 TATCGGGGGGGACGGGGCGGTGGTAATTACAAGCGAGATCTCGAGAAC
2351 TTGTTGGGAACTCAGGGCATCTGATCCCGCCGCCCCACATGGAATGGAGCTG
2401 GGTCTTCTCTCTCCGTCAAGTAACACTACAGGTGTCCACTCCGACATCC
2451 AGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTC
2501 ACTATCACATGTGAGCAAGTGGGAATTTCACAATTATTAGCATGGTA
2551 TCAGCAGAACAGGGAAAATCTCTCAGCTCTGGTCTATAATGCAAAA
2601 CCTTAGCAGATGGTGTGCCATCAAGGTTCAAGGTTCAAGGGATCAGGAACA
2651 CAATATTCTCTCAAGATCAACAGCCTGCAGGCTGAAGGATTGGGAGTTA
2701 TTACTGTCAACATTGGAGTACTCCGTGGACGTTGGTGGAGGGCACCA
2751 AGCTGGAAATCAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCA
2801 CCATCCAGTGAGCAGTAACATCTGGAGGTGCTCAGTCGTGCTTCTT

Figure 11b

2851 GAACAACCTTCTACCCCAAAGACATCAATGTCAGTGGAAAGATGATGGCA
2901 GTGAACGACAAAATGGCGTCTGAACAGTTGGACTGATCAGGACAGCAAA
2951 GACAGCACCTACAGCATGAGCAGCACCCCTCACATTGACCAAGGACGAGTA
3001 TGAACGACATAACAGCTATACTGTGAGGCCACTCACAAGACATCAACTT
3051 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTGAAAGCATCGATTT
3101 CCCCTGAATTGCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAA
3151 GCCGCTTGGAAATAAGGCCGTGCGTTGTCTATATGTTATTTCCACC
3201 ATATTGCCGTCTTGCAATGTGAGGGCCGAAACCTGGCCCTGTCTT
3251 CTTGACGAGCATTCTAGGGTCTTCCCCTCTGCCAAAGGAATGCAAG
3301 GTCCTGGAATGCTGTAGCAGCCCTTGCAAGGCAGTTCTCTGGAAAGCTTCTGAAGA
3351 CAAACAACGTCGTAGCAGCCCTTGCAAGGCAGCGAACCCCCCACCTGG
3401 CGACAGGTGCCCTTGCGGCCAAAAGCCACGTGTATAAGATAACACCTGAA
3451 AGGGGGCACAACCCCAGTCCACGTTGTGAGTTGGATAGTTGTGGAAAGA
3501 GTCAAATGGCTCTCTCAAGCTTCAACAAGGGCTGAAGGGATGCCA
3551 GAAGGTACCCCATGATGGGATCTGATCTGGGCTCGGTCCACATGCT
3601 TTACATGTGTTAGTCGAGGTTAAAAAAACGTCAGGCCCCCGAACAC
3651 GGGGACGTGGTTCTTCTGGTAAAGAACACGATGATAATATGGCTCCTTG
3701 TCTCTGCTCTGGTAGGCATCTTCAATGCCCCAGGCCAGGGTT
3751 CAGCTTCAGCAGTCTGGGGCAGAGCTGTGAAGCCAGGGCTCAGTCAA
3801 GTTGTCTGCACAGCTCTGGCTTCAACATTAAGACACCTTATGCACT
3851 GGGTGAAGCAGAGGCCCTGAACAGGGCTGGAGTGGATTGGAAGGATTGAT
3901 CCTCGAATGGAATACTGAATATGACCCGAAGTCCAGGGCAAGGCCAC
3951 TATAACAGCAGACACATCCTCAACACAGTCACCTGCAGCTCAGCAGCC
4001 TGACATCTGAGGGACACTGGCTCTATTACTGTGCTAGTGGAGGGAACTG
4051 GGGTTCTTACTGGGCAAGGGACTCTGGTCAGTCTCTGCAGCCAA
4101 AACGACACCCCCATCTGCTATCCACTGGGCCCTGGATCTGTCAGCCAAA
4151 CTAACCTCATGGTGACCCCTGGGATGCTGGTAAAGGCTATTCCCTGAG
4201 CCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCAGCGGTGTGCACAC
4251 CTTCCCAGCTCCTGCAGTTGACCTCTACACTGAGCAGCTCAGTGA
4301 CTGTCCTCCAGCACCTGGCCAGCAGCACCTGGGATGCTGGTAAACCGT
4351 CACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGTGCCAGGGATTG
4401 TACTAGTGGAGGTGGAGGTAGGCCACCATCACCATTAAATCTAGAG
4451 TTAAGGGGCCCTGGAGATCTGACATCGATAATCAACCTCTGGATTACAA
4501 AATTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCTTTACGC
4551 TATGTGGATACGCTGCTTAAATGCCCTTGATCATGCTATTGCTTCCCGT
4601 ATGGCTTCATTTCTCCCTTGATATAAATCTGGTTGCTGTCTTTA
4651 TGAGGAGTTGTGGCCCGTGTCAAGGAAACGTGGCGTGGTGTGCACTGTG
4701 TTGCTGACGCAACCCCCACTGGTTGGGCATTGCCACCCCTGTCAGCTC
4751 CTTTCCGGGACTTTGCTTCCCCCTCCATTGCCACGGCGGAACCTCAT
4801 CGCCGGCTGCTTGGCCCTGCTGGACAGGGCTCGGCTGTGGGACTG
4851 ACAATTCCGTGGTGTGTCAGGGAAATCATGCTCTTCTGGCTGCTC
4901 GCCTGTGTTGCCACCTGGATTCTGCCGGGACGTGCTTCTGCTACGTCCC
4951 TTCCGGCCCTCAATCCAGCGGACCTTCTTCCCGGGCTGCTGCCGGCTC
5001 TGCGGCCCTTCCCGCTTCCGCTGCTGCCCTCAGACGAGTCGGATCTCC
5051 CTTGGGGCGCTCCCCGCTGATCGATAAAATAAAGATTATTAGT
5101 CTCCAGAAAAGGGGGAAATGAAAGACCCCCACCTGTAGGTTGGCAAGCT
5151 AGCTTAAGTAACGCCATTGCAAGGCATGGAAAAAAATACATAACTGAGAA
5201 TAGAGAAGTTAGATCAAGGTCAAGGAACAGATGGAACAGCTGAATATGGG
5251 CCAAAACAGGATATCTGGTAAGCAGTTCTGCCCGCTCAGGGCAAG
5301 AACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGGTAAGCA
5351 GTTCCCTGCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCCGGTCC
5401 AGCCCTCAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGGCCCAA
5451 GGACCTGAAATGACCCCTGTGCCTTATTGAAACTAACCAATCAGTTCGCTT
5501 CTCGCTCTGTTCGCGCCTCTGCTCCCCGAGCTCAATAAAAGAGGCCA
5551 CAACCCCTCACTCGGGGCCAGTCTCCGATTGACTGAGTCGCCGGGT
5601 ACCCGTGTATCCAATAAACCTCTTGCAGTTGCATCCGACTTGTGGTCTC

Figure 11c

5651 GCTGTTCCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGG
5701 GGTCTTCATT

1 - 2053	Bovine/human alpha-lactalbumin 5' flanking region
2093 - 2336	Double mutated PPE sequence
2387 - 2443	cc49 signal peptide coding region
2444 - 3088	Bot antibody light chain Fab coding region
3112 - 3686	EMCV IRES
3687 - 3745	Bovine alpha-lactalbumin signal peptide coding region
3746 - 4443	Bot antibody heavy chain Fab coding region
4481 - 5072	WPRE sequence
5118 - 5711	Moloney murine leukemia virus 3' LTR

Figure 12a
SEQ ID NO:9
LSNRL Vector

1 TTTGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT
51 TGCAAGGCATGGAAAAAATACATAACTGAGAAATAGAAAAGTCAGATCAAG
101 GTCAGGAACAAAGAAACAGCTGAATACCAACAGGATATCTGTGGTAAGC
151 GGTTCCTGCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATG
201 GGCCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCGGCTCGGGGCCA
251 AGAACAGATGGTCCCCAGATGCGGCCAGCAGTTCTAGTGAA
301 TCATCAGATGTTCCAGGGTGCCAACAGGACCTGAAAATGACCTGTACC
351 TTATTGAACTAACCAATCAGTTCGTTCTCGCTTCTGTTCGCGCCTTC
401 CGCTCTCGAGCTCAATAAAAGAGGCCAACACCCCTCACTCGGCCGCCA
451 GTCTCCGATAGACTGCCCGGGTACCCGATTCCCAATAAGCCT
501 CTGCTGTTGATCCGAATCGTGGTCTCGCTGTTCTGGAGGGTCTC
551 CTCTGAGTGAATGACTACCCACGACGGGGTCTTCATTGGGGGCTCGT
601 CCGGGATTGGAGACCCCTGCCAGGGACCACCGACCCACCGGGAGG
651 TAAGCTGCCAGCAACTTATCTGTGTCTGCCATTGTCTAGTGTCTATG
701 TTTGATGTTATGCGCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTAT
751 CTGGCGGACCCGTGGTGAACGTGACGGAGTTCTGAACACCCGGCGAAC
801 CTGGGAGACGCTCCAGGGACTTTGGGGCCGTTTGTGGCCCGACCTGA
851 GGAAGGAGTCGATGTGAATCCGACCCCGTCAGGATATGTGGTTCTGGT
901 AGGAGACGAGAACCTAAACACTTCCCGCTCCGCTGAATTGGCTTT
951 CGGTTGGAACCGAAGCCGCGTCTTGTCTGCTGAGCAAGCTGGGC
1001 TCGAGGTGAGGACTGGGACCCCTGCCTGTTACAGGGGGTTTTCTTGTGA
1051 AGGATTCTAGGACCCCTGCTGTGTTACAGGGGGTTTTCTTGTGA
1101 CAAGAACCTCACAATACCACAGAGTCAAGACTCGTGTGGACTTCTC
1151 AATTTCTAGGGGAGCACCCACGTGCTGGCAAATTCGAGTCCCC
1201 AACCTCCAATCACTCACCAACCTCTGTGCTTCAATTGTCCCTGGCTATC
1251 GCTGGATGTGCTGCCGGGTTTATCATATTCTCTCATCCTGCTGCTA
1301 TGCCCTCATCTTCTGTTGGTCTCTGGACTACCAAGGTATGTTGCCGT
1351 TTGCTCTACTTCCAGAACATCAACTACCAAGCACGGGACCATGCAAGA
1401 CCTGCACGATTCTGCTCAAGGAACCTCTATGTTCCCTCTGTTGCTGT
1451 ACAAAACCTCGGACGAAACTGCACCTGTTATCCCATCCATCCTG
1501 GGCTTCGCAAGATTCTATGGGAGTGGGCTCAGTCCGTTCTCCTGGC
1551 TCAGTTTACTAGTGCCTTGTGTTAGTGGCTAGGGCTTCCCCCACT
1601 GTTGGCTTCAAGTTATGGATGATGTTGTTGGGAGGGCCAAGTCTGTA
1651 CAACATCTTGAGTCCCTTTACCTCTATTACCAATTTCCTTGTCTT
1701 GGGTATACATTAAACCTAATAAAACCAAACGTTGGGGCTACTCCCTTA
1751 ACTTCATGGATATGTAATTGGATGTTGGGGTACTTTACCGCAAGAACAT
1801 ATTGTACTAAAATCAAGCAATTGTTGCCAAACTGCCTGAAATAGACC
1851 TATTGATTGAAAGTATGTCAGAGACTTGTGGCTTTGGGCTTGTG
1901 CCCCTTTACACAATGTGGCTATCTGCCCTAATGCCCTTATATGCATGT
1951 ATACAATCTAACGAGGCTTCACTTCTGCCAACCTAACAGGCCTTCT
2001 GTGTAACAAATCTGAACCTTACCCCGTGGGGCTTGGCTATC
2051 TCTGCCAAGTGTGCTGACGCCAACCCCACTGGATGGGCTTGGCTATC
2101 GGGCATAGCCGATGCCGGACCTTGTGGCTCTCGCCGATCCATACT
2151 GCGGAACCTCTAGCAGCTGTTGCTCGCAGGGCTGGAGCGAAACT
2201 TATGGCACCGACAACCTGTTGCTCTCTCGGAAATACACCTCTTTC
2251 CATGGCTGCTAGGGTGTGCTGCCAAGTGGATCCCTCAGGATATAGTAGT
2301 TTCGCTTGTGATAGGGAGGGGAAATGTAAGCTTATGCAATTACACTTGT
2351 AGTCTGCAACATGGTAACGATGAGTTAGCAACATGCCCTACAAGGAGAG
2401 AAAAGCCTGCGATGCCGATGGTGGAAAGTAAGGTGGTACGATGTGC
2451 CTTATTAGGAAGGCAACAGACAGGCTGACATGGATGGAGCAACCACTG
2501 AATTCCGCATTGCAAGAGATAATTGTATTAAAGTGCCTAGTCGATACAGC
2551 AAACGCCATTGGACCATTCACCAACATTGGTGTGCACCTTCCAAAGCTT
2601 CACGCTGCCGCAAGCACTCAGGGCGCAAGGGCTGCTAAAGGAAGCGGAAC
2651 ACGTAGAAAGCCAGTCGCAGAAACGGTGTGACCCGGATGAAATGTCAG
2701 CTACTGGGCTATCTGGACAAGGGAAAACGCAAGCGCAAAGAGAAAGCAGG
2751 TAGCTTGCAGTGGCTACATGGCAGTAGCTAGACTGGGGTTTATGG
2801 ACAGCAAGCGAACCGGAATTGCCAGCTGGGGGCCCTCTGGTAAGGTGG

Figure 12b

2851 GAAGCCCTGCAAAGTAAACTGGATGGCTTCTTGCAGGCCAAGGATCTGAT
2901 GGCGCAGGGATCAAGATCTGATCAAGAGACAGGATGAGGATCGTTCGC
2951 ATGATTGAACAAGATGGATTGCACGCAGGTCTCCGGCCGTTGGGTTGGA
3001 GAGGCTATTGGCTATGACTGGGCACAAACAGACAATCGGCTGCTGATG
3051 CGGCCGTGTCGGCTGTCAGCGCAGGGCGCCGGTTCTTTGTCAG
3101 ACCGACCTGTCGGTGCCTGAATGAACACTGCAGGACGAGGCAGCGCGCT
3151 ATCGTGGCTGGCACGACGGCGTCCCTGCGCAGCTGCTGACGTTG
3201 TCAGTAAGCGGAAGGGACTGGCTATTGGCGAAGTGCCCAGGGCAG
3251 GATCTCTGTCATCTCACCTGCTCTGCGAAGAAAGTATCCATCATGGC
3301 TGATGCAATCGCCGGCTGTCATCGCTGATCCGCTACCTGCCATTG
3351 ACCACCAAGCGAACATCGCATCGAGCGAGCACGTAACCGGATGGAAGCC
3401 GGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGCGCC
3451 AGCCGAACGTTCGCCAGGCTAAGGCAGCGATGCCGACGGCAGGATC
3501 TCGTGTGACCCATGGCGATGCTGCTTGCGAATATCATGGTGGAAAAT
3551 GGCCTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCG
3601 CTATCAGGACATAGCGTTGGCTACCCCGTATTTGCTGAAGAGCTGGG
3651 GCGAATGGGCTGACCCTCTCGTGTCTTACGGTATCGCCGCTCCCGAT
3701 TCGCAGCGCATGCCCTCATCGCTTCTGACGAGTTCTCTGAGCGGG
3751 ACTCTGGGTTGCAAATGACCGACCAAGCGACGCCAACCTGCCATCAC
3801 AGATTCGATTCCACGCCCTCTATGAAAGGGTGGGCTTCGGAATCG
3851 TTTCCGGGACGCCGGCTGGATGATCCTCAGCGCGGGGATCTCATGCTG
3901 GAGTTCTGCCACCCCAACCCCTGGCTATTATTGGGTGGACTAACCA
3951 TGGGGGAATTGCCGCTGAAATAGGAACAGGGACTACTGCTCTAATGGCC
4001 ACTCAGCAATTCCAGCAGCTCAAGCCCGAGTACAGGATGATCTCAGGG
4051 GGTGAAAATCAATCTCTAACCTAGAAAAGTCTCATCTACTCCCTGCTG
4101 AAGTGTCTACAGAACGGGCTAGACTTGTATTCTAAAAGAA
4151 GGAGGGCTGTGCTGCTCTAAAGAAGATGTTGCTTCTATGCCGACCA
4201 CACAGGACTAGTGGAGAGACAGCATGCCAATTGAGAGAGAGGGCTTAATC
4251 AGAGACAGAAAATGTTGAGTCACACTAAGGATGTTGAGGGACTGTTT
4301 AACAGATCCCCCTGGTTTACACCTTGATATCTACCATTATGGGACCCCT
4351 CATGTACTCTAAATGATTTGCTCTCGGACCTGCTTAAATCGAT
4401 TAGTCCAATTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTT
4451 ACTCAACAATATCACCAGCTGAAGCTATAGACTACAGGCCATAGATAAA
4501 ATAAAAGATTTATTAGTCTCCAGAAAAAGGGGGATGAAAGACCCCA
4551 CCTGTAGGTTGGCAAGCTAGCTTAAGTAACGCCATTGCAAGGCATGG
4601 AAAATACATAACTGAGAATAGAGAAGTTCAAGATCAAGGTAGGAACAGA
4651 TGGAACAGCTGAATATGGCCAAACAGGATATCTGTGGTAAGCAGTTCC
4701 GCCCGGCTCAGGCCAAGAACAGATGGAACAGCTGAATATGGCCAAAC
4751 AGGATATCTGTGGTAAGCAGTCTGCCCCGGCTCAGGGCCAAGAACAGA
4801 TGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTCTAGAGAACCATCAGA
4851 TGGTCCAGGGTGCCCAAGGACCTGAAATGACCTGTGCCTTATTGAA
4901 CTAACCAATCAGTCGCTCTCGCTCTGTCGCGCTCTGCTCCCCG
4951 AGCTCAATAAAAGAGGCCACAACCCCTCACTGGGGGCCAGTCCTCCGA
5001 TTGACTGAGTCGCCCGGGTACCCGTGATCCAATAAAACCTCTTGCAGTT
5051 GCATCCGACTGTGGTCTCGCTTCTGGGAGGGTCTCCTCTGAGTGA
5101 TTGACTACCCGTCAGCGGGGGCTTTCATT

- 1 - 589 MoMuSV 5' LTR
659 - 897 Retroviral packaging region
1034 - 1714 Hepatitis B surface antigen
2279 - 2595 RSV promoter
2951 - 3745 Neomycin phosphotransferase gene
4537 - 5130 MoMuLV 3' LTR

Figure 13a
SEQ ID NO:10
Alpha-Lactalbumin cc49IL2 Vector

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1 GATCAGTCCTGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51 AATACTTTGGCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCCTG
101 ATACTGGGAAAGATTGAAGGCAGGAGAGAAGGGATGACAGAGGATGGAA
151 GAGTTGGATGGAATCACCACACTCGATGCCATGAGTTGAGCAAGCTTCC
201 AGGAGTTGGTAATGGCGAGGAAAGCCTGGCGTCTGCAGTCCATGGGGTT
251 GCAGAAGAGTTGGACACTACTGAGTGAACGTGAACTGATAGTGTAAATC
301 CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGGTTGCCCTGATTCTG
351 AAGAGTTGAGGATATAAAAGTTAGAATACCTTAGTTGAAAGTCTTA
401 ATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451 AGAGACTGATGTAGAGAGAATGAGCCTGGCATACCAGAAGCTAACAGCT
501 ATTGGTTATAGCTGTTATAACCAATATAACCAATATATTGGTTATATA
551 GCATGAAGCTTGATGCCAGCAATTGAGGAACCATTTAGAACTAGTATC
601 CTAACACTACATGTTCCAGGACACTGATCTAAAGCTCAGGTTCAGAAT
651 CTTGTTTATAGGCTTAGGTGTATATTGTGGGCTTCCCTGGTGTCA
701 GATGGTAAAGTGTCTGCTGCAATGTGGGTGATCTGGGTTGATCCCTGG
751 CTTGGGAAGATCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801 ACCTGGAAAATCCATGGACAGAGGAGCCTGTAAGCTACAGTCCATGGG
851 ATTGCAAAGAGTTGAACACAACGTGAGCAACTAACGACAGCACAGTACAGT
901 ATACACCTGTGAGGTGAAGTGAAGGTTCAATGCAGGGCTCCTG
951 ATTGCAAGAAAGATTCTTACCATCTGAGGCCACCGAGGAAAGCCAAGATA
1001 CTGGAGTGGTAGCCTATTCTCCTCCAGGGGATCTTCCCCTCCAGGAA
1051 TTGAACCTGGAGTCTCCTGCAATTTCAGGTGGATTCTCACCAAGCTGAAC
1101 CCAGGTGGATACTACTCCAATATTAAGTGTCTAAAGTCCAGTTTCCC
1151 CCTTCCCAAAAAGGTTGGTCACTCTTTAACCTTCTGTGGCCTACT
1201 CTGAGGCTGTCTACAAGCTTATATATTATGAACACATTTATTGCAAGTT
1251 GTTAGTTTAGATTTACAATGTGGTATCTGGCTATTAGTGGTATTGGTG
1301 GTTGGGGATGGGAGGGTGTAGCATCTCAGAGGGCAGCTAGATACTGTC
1351 ATACACACTTCAAGTTCTCCATTTTGTGAAATAGAAAAGTCTCTGGAT
1401 CTAAGTTATATGTGATTCTCAGTCTGTGGTCAATTCTATTCTACTCC
1451 TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTGTTGTTCA
1501 TGCCTGGGTGAGTGGGCATGACATATGTTGGGCTTGTACATGGC
1551 TGATTGGTGGACAAGTGCAGCTGTGATCCTGGACTGTGGCATGTGA
1601 TGACATACACCCCTCTCACATTCTGCATGTCCTAGGGGGAAAGGGGG
1651 AAGCTCGGTATAGAACCTTATTGTATTCTGATTGCCTCACTTCTTAT
1701 ATTGCCCCCATGCCCTTGTGTCCTCAAGTAACCCAGAGACAGTGCCTC
1751 CCAGAACCAACCCCTACAAGAAACAAAGGGCTAACAAAGCCAATGGGA
1801 GGAGGATCATGGTTGAACCTTTCTGGCCAGAGAACAAATACCTGCTATG
1851 GACTAGATACTGGGAGAGGAAAGGAAAGTAGGGGTGAATTATGGAAGGA
1901 AGCTGGCAGGCTCAGCCTTCTGTCTGGCATGACCAGTCTCTTCTCATT
1951 CTCTCCCTAGATGTAGGGCTTGGTACCAAGAGCCCTGAGGCTTCTGCA
2001 GAATATAAAATATGAAACTGAGTGTATGCTTCCATTTCAGGTTCTGGG
2051 GCGCGAATTGAGCTGGTACCCGGGATCTCGAGAAGCTTAACCATG
2101 GAATGGAGCTGGCTTCTCTCTCTGTCACTGAAACTACAGGTGTCCA
2151 CTCAGGTTCAAGTCAGCAGTCTGACGCTGAGTTGGTGAACACCTGGG
2201 CTCAGTGAAGATTCTCTGCAAGGCTTCTGGCTACACCTTCACTGACCAT
2251 GCAATTCACTGGTGAACAGAACCTGAACAGGGCTGGAAATGGATTGG
2301 ATATTTCTCCGGAAATGATGATTTAAATACAATGAGAGGTTCAAGG
2351 GCAAGGCCACACTGACTGCAGACAAATCTCCAGCACTGCCTACGTGCA
2401 CTCACAGCCTGACATCTGAGGATTCTGCAGTGTATTCTGTACAAGATC
2451 CCTGAATATGCCACTGGGCTAAGGAACCTCAGTCACGGCTCTCAG
2501 GAGGGGGAGGCAGGGAGGGGGTGGCTCGGGAGGCGGAGGCTGGACATT
2551 GTGATGTCACAGTCTCCATCTCCCTACCTGTGTCAGITGGCGAGAAGGT
2601 TACTTGAGGCTGCAAGTCCAGTCAGAGCCTTATATAGTGGTAATCAA
2651 AGAACTACTGGCCTGGTACCAAGAGAAACCAAGGGCAGTCTCTAAACTG
2701 CTGATTTACTGGGACATCGCTAGGAATCTGGGTCCCTGATCGCTTCA
2751 AGGCAGTGGATCTGGGACAGATTCACTCTCCATCAGCAGTGTGAAGA
2801 CTGAAGACCTGGCAGTTATTACTGTCAGCAGTATTAGCTATCCCCTC

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Figure 13b

2851 ACGTTGGTCTGGGACCAAGCTGGTCTGAAACGGGCCGAGCCCAA
2901 ATCTCCTGACAAAACTCACACATGCCACCGTGCAGCACCTGAACCTCC
2951 TGGGGGGACCGTCAGTCTTCCCTTCCCCAAAACCCAAGGACACCCCTC
3001 ATGATCTCCGGACCCCTGAGGTACATGCGTGGTGGACGTGAGCCA
3051 CGAAGACCCCTGAGGTCAAGTCAACTGGTACGTGACGGCGTGGAGGTGC
3101 ATAATGCCAAGACAAGCCGGAGGAGCAGTACAACAGCACGTACCGT
3151 GTGGTCAGCGTCTCACCCTGACCCAGGACTGGCTGAATGGCAAGGA
3201 GTACAAGTGAAGGTCTCAACAAAGCCCTCCAGCCCCATCGAGAAAAA
3251 CCATCTCCAAAGCCAAGGGCAGCCCCAGAACACAGGTGTACACCCCTG
3301 CCCCCATCCGGATGAGCTGACCAAGAACCCAGGTCAAGCTGACCTGCCT
3351 GGTCAAAGGCTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATG
3401 GGCAGCCGGAGAACAACTACAAGACCAAGCCTCCCGTGTGGACTCCGAC
3451 GGCTCCTTCTTCCCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCA
3501 GCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC
3551 ACTACACGCAGAAGAGCCTCTCCCTGTCCTCCGGTAAAGGAGGCCGATCA
3601 GGAGGTGGCGCACCTACTTCAAGTTCTACAAAGAAAACACAGCTACAAC
3651 GGAGCATTACTGCTGGATTACAGATGATTGAAATGGAATTATAATT
3701 ACAAGAATCCAAAACCTCAGGATGTCACATTAAAGTTTACATGCC
3751 AAGAAGGCCACAGAACTGAAACATCTCAGTGTCTAGAAGAAGAACTCAA
3801 ACCTCTGGAGGAAGTGCTAAATTAGCTCAAAGCAAAACTTCACTTAA
3851 GACCCAGGGACTTAATCAGCAATATCAACGTAATAGTTCTGAACTAAAG
3901 GGATCTGAAACAACATTATGCTGTAATATGCTGATGAGACAGCAACCAT
3951 TGTAGAATTCTGAACAGATGGATTACCTTTGTCAAAGCATCTCAA
4001 CACTAACTTGAAGCTGTAAACATCGATAAAATAAAAGATTATTAGT
4051 CTCAGAAAAAAGGGGGAAATGAAAGACCCACCTGTAGGTTGGCAAGCT
4101 AGCTTAAGTAACGCCATTGCAAGGCATGGAAAATACATAACTGAGAA
4151 TAGAGAAGTTCAGATCAAGGTCAAGGAACAGATGGAACAGCTGAATATGGG
4201 CCAACAGGATATCTGTGTAAGCAGTCTGCCCGGCTCAGGGCAAG
4251 AACAGATGGAACAGCTGAATATGGCCAAACAGGATATCTGTGTTAAGCA
4301 GTTCTGCCCCGGCTCAGGCCAAGAACAGATGGTCCCCAGATGCGGTCC
4351 AGCCCTCAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGGCCCAA
4401 GGACCTGAAATGACCCCTGTGCCTTATTGAACTAACCAATCAGTCGCTT
4451 CTCGCTTCTGTTCCGGCCCTCTGCTCCCCGAGCTAATAAAAGAGCCCA
4501 CAACCCCTCACTCGGGCGCCAGTCCTCGATTGACTGAGTCGCCGGGT
4551 ACCCGTGTATCCAATAAACCCCTTTCGAGTTGCACTCCGACTTGTGGTCTC
4601 GCTGTTCTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTAGCGGG
4651 GGTCTTTCAT

1 - 2055 Bovine/human alpha-lactalbumin 5' flanking region

2098 - 4011 cc49-IL2 coding region

4068 - 4661 MoMuLV 3' LTR

Figure 14a
SEQ ID NO:11
Alpha-Lactalbumin YP Vector

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1      GATCAGTCCTGGTGGTCAATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51     AATACTTTGGCACCTGATGCGAAGAACGTGACTCATGTGATAAGACCCCTG
101    ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151    GAGTTGGATGGAATCCAACACTCGATGGACATGAGTTGAGCAAGCTTCC
201    AGGAGTTGTAATGGGAGGGAGGCTGGCGTGCAGTCCATGGGTT
251    GCAAAGAGTTGACACTACTGAGTGACTGAACGTGATAGTGAATC
301    CATGGTACAGAATATAGGATAAAAAGAGGAAGAGGTTGCCCTGATTCTG
351    AAGAGTTGAGGATATAAAAGTTAGAATACCTTAGTTGAAGTCTTA
401    AATTATTTACTTAGGATGGTACCCACTGCAATAAGAAATCAGGTTT
451    AGAGACTGATGAGAGAATGAGCCCTGGCATACCAGAACGTAACAGCT
501    ATTGGTTAGCTGTTAACCATAAACCAATTGGTTATATA
551    GCATGAAGCTTGTGCGCACATTGAGGAACATTAGAACTAGTATC
601    CTAACACTCATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651    CTTGTTTATAGGCTCTAGGTGTATATTGTTGGGCTTCCCTGGCTCA
701    GATGGTAAAGTGTCTGCCGCAATGTTGGGTGATCTGGGTCATCCCTGG
751    CTTGGGAAAGATCCCCTGGAGAAGGAAATGCCAACCCACTCTAGTACTCTT
801    ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAAGCTACAGTCCATGGG
851    ATTGCAAAAGAGTTGAAACACAACGCAACTAACGACACAGTACAGT
901    ATACACCTGTGAGGTGAAGTGAAAGTCAATGCAAGGCTCTCCTGC
951    ATTGAGAAAGATTCTTACCATCTGAGCCACCCAGGGAAAGCCAAGAATA
1001   CTGGAGTGGGTAGCCTATCCTCTCCAGGGATCTTCCATCCCAGGAA
1051   TTGAACTGGAGTCTCCTGCATTTCAAGGTGGATTCTCACCAAGCTGAAC
1101   CCAGGTGGATACTACTCCAATATTAAAGTCTTAAAGTCCAGTTTCCCA
1151   CCTTCCAAAAGGTTGGTCACTCTTTTAACCTTCTGTTGGCTACT
1201   CTGAGGTGCTACAAGCTTATATATTTGAAACACATTATGGCAAGTT
1251   GTTAGTTTGGATTTACAATGTGGTATCTGGCTATTAGTGGTATTGGT
1301   GTTGGGGATGGGGAGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351   ATACACACTTTCAAGTCTCCATTGGTAAAGTCAACAGTCTCTGGAT
1401   CTAAGTTATATGTGATTCTCAGTCTGTGGTCATATTCTATTCTACTCC
1451   TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTGTTGTTCA
1501   TGCCTGGGTGAGTGGCCATGACATATGTTCTGGCTTACATGGC
1551   TGGATTGGTGGACAAGTGCCAGCTGATCTGGGACTGTGGCATGTGA
1601   TGACATACACCCCTCTCCACATTGCACTGTCTAGGGGGAAAGGGGG
1651   AAGCTGGTATAGAACCTTATTGTATTCTGATTGCTCAGTCTTAT
1701   ATTGCCCCATGCCCCCTTCTTGTCTCAAGTAACCAAGAGACAGTCTTC
1751   CCAGAACCAACCCCTACAAGAAACAAGGGCTAACAAAGCCAAATGGGAA
1801   GCAGGATCATGGTTGAACCTCTCTGGCCAGAGAACAAACCTGCTATG
1851   GACTAGATACTGGGAGAGGGAAAGGAAAGTAGGGTGAATTATGGAAGGA
1901   AGCTGGCAGGCTCAGCGTTCTGTCTGGCATGACCAAGTCTCTTCATT
1951   CTCTTCCCTAGATGTAGGCTTGGTACCAAGAGCCCTGAGGCTTCTGCA
2001   GAATATAAAATATGAAACTGAGTGATGCTTCAATTGAGGTTCTGGG
2051   GCGCCGAATTGAGCTGGTACCCGGGATCTGGCATGGGATCCGAGGATCCGATT
2101   ACTGGCAGGTGCTGGGCTTCCGAGAACATCGGAACATCTACACCA
2151   CAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGACGCCGGTGGT
2201   AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGCTTCCGA
2251   GACAATCGCGAACATCTACACCACACAACCCGCTCGACCAGGGTGAGA
2301   TATCGGCCGGGACCGCGGGTGGTAAATTACAACCGAGATCTCGAGTTAA
2351   CAGATCTAGGCCCTCTAGGTGACGGATCCCCGGGAAATTGGCGCCG
2401   CCATGATGCTCTTGTCTCTGCTCTGGTAGGCATCCTATTCCATGCC
2451   ACCCAGGCCAGGTCCAACACTGCAGCAGTCTGGCCTGAGCTGGTGAAGCC
2501   TGGGACTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAA
2551   GCTACTATTACACTGGGTAAGCAGAGGCCGGACAGGGACTTGAGTGG
2601   ATTGCATGGATTATCTGGAAATGTTATTACTACGTACAATGAGAAGTT
2651   CAAGGGCAAGGCCACACTGACTGCAGACAAATCTCCAGCACAGCCTACA
2701   TGCACCTCAACAGCCTGACCTGTAGGACTCTGGGTCTATTCTGTGCA
2751   AGGGGTGACCATGATCTGACTACTGGGCAAGGCACCAACTCTCACAGT
2801   CTCCCTAGCAGCAAAAGCACACCCCCATCTGTCTATCCACTGGCCCTGGAT

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Figure 14b

2851 CTGCTGCCAAACTAACTCCATGGTACCCCTGGGATGCCTGGTCAGGGC
2901 TATTCCCTGAGCCAGTGACAGTGACCTGGAACCTCTGGATCCCTGTCCAG
2951 CGGTGTGCACACCTTCCCAGCTGTCTGCAGTCTGACCTCTACACTCTGA
3001 GCAGCTCAGTGACTGTCCCCCTCCAGCACCTGGCCAGCGAGACCGTCACC
3051 TGCAACGTTGCCAGGGCCAGCAGCACCAAGGTGGACAAGAAAATTGT
3101 GCCCAGGGATTGTACTAGTGGAGGTGGAGGTAGCTAAGGGAGATCTCGAC
3151 GGATCCCCGGGAATTCCGCCCCCTCTCCCCCCCCCTAACGTTACTGG
3201 CCGAAGCCGCTTGAATAAGGCCGGTGTGCGTTGTCTATATGTTATTT
3251 CCACCATATTGCCGTCTTGGCAATGTGAGGGCCGGAAACCTGGCCCT
3301 GTCTTCTGACGAGCATTCTAGGGTCTTCCCCCTCGCCAAAGGAAT
3351 GCAAGGTCTGTGAATGTGTAAGGAAGCAGTTCTCTGGAAAGCTTCTT
3401 GAAGACAAACAACGTCTGTAGCGACCTTTGCAGGCAGCGGAACCCCCCA
3451 CCTGGCGACAGGTGCCTCTGCCGGCAAAGCCACGTGTATAAGATAACCC
3501 TGCAAAAGGCCACAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGG
3551 AAAAGACTCAATGGCTCTCTCAAGCGTATTCAACAAAGGGCTGAAGGAT
3601 GCCCAGAAGGTACCCCATGTATGGGATCTGATCTGGGGCCTCGGTGAC
3651 ATGCTTACATGTGTTACTCGAGGTAAAAAAACGCTTAGGCCCGGGCGA
3701 ACCACGGGACGTGGTTTCTTGGAAAAACACGATGATAATATGGCCTC
3751 CTTGTCCTCTGCTCTGGTAGGCATCCTATTCCATGCCACCCAGGCCG
3801 ACATTGTGCTGACACAATCTCAGCAATCATGTCGATCTCCAGGGGAG
3851 AAGGTACCATGACCTGCACTGCAGTCAGGCCACCTCAAGTGTAAGTTACATACACTG
3901 GTACCAGCAGAAGTCAGGCCACCTCCCCAAAAGATGGATTATGACACAT
3951 CCAAACGGCTCTGGAGCTCTGCTCGCTTCAGTGGCAGTGGGTCTGGG
4001 ACCTCTCACTCTCACACTCAGCAGCATGGAGGTGAAGATGCTGCCAC
4051 TTATTACTGCCAGCAGTGGGGTAGTTACCTCACGTTCGTGCAGGGGACCA
4101 AGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCA
4151 CCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTTGCTTCT
4201 GAACAACCTCTACCCCAAAGACATCAATGTCAGTGGAGGAAAGATTGATGGCA
4251 GTGAAACGACAAAATTGGCTCTGAACAGTTGGACTGATCAGGACAGCAA
4301 GACAGCACCTACAGCATGAGCAGCACCTCACGTTGACCAAGGACGAGTA
4351 TGAACGACATAACAGCTATACTGTGAGGCCACTACAAGACATCAACTT
4401 CACCCATTGTCAGAGCTCAACAGGAATGAGTGTAAATAGGGGAGATCT
4451 CGACATCGATAATCAACCTCTGGATTACAAAATTGTGAAAGATTGACTG
4501 GTATTCTTAACATATGTTGCTCTTACGCTATGGGATACGCTGCTTTA
4551 ATGCCCTTGATCATGCTATTGCTTCCCGTATGCTTTCATTTCTCTC
4601 CTTGTTAAATCTCTGGTGTCTCTCTTATGAGGGAGTTGTGGCCCGTTG
4651 TCAGGCAACGGCTGGCTGTGACTGTGTTGCTGACGCAACCCCCACT
4701 GTTGGGGCATTGCCACCCACTGTAGCTCCCTTCCGGGACTTCGCTTT
4751 CCCCTCCCTATTGCCACGGCGGAACTCATGCCGCTGCCCTGCCGCT
4801 GCTGGACAGGGGCTGGCTGTTGGCACTGACAAATTCCGTGGTGTGTCG
4851 GGGAAATCATGTCCTTCTGGCTGCTGCCGTGTTGCCACCTGGAT
4901 TCTGCGGGACGTCTCTGCTACGTCCCTTCCGGCCCTCAATCCAGCGG
4951 ACCCTCCCTCCCGCGGCCCTGCTGCCGCTCTGCCGCTCTCCGCTCTT
5001 CGCCCTCGCCCTCAGACGAGTCGGATCTCCCTTTGGCCGCTCCCCGCC
5051 TGATCGATAAAAATAAAAGATTTTATTAGTCTCAGAAAGGGGGGAAT
5101 GAAAGACCCCACCTGTAGGTTGGCAAGCTAGCTTAAGTAACGCCATT
5151 GCAAGGCATGAAAAATACATAACTGAGAATAGAGAAGTTAGATCAAGG
5201 TCAGGAACAGATGGAACAGCTGAATATGGCCAAACAGGGATATCTGTGGT
5251 AAGCAGTCCCTGCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAAT
5301 ATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCGGCTCAGGG
5351 CCAAGAACAGATGGTCCCCAGATGCCGTCCAGGCCCTCAGCAGTTCTAGA
5401 GAACCATCAGATGTTCCAGGGTCCCCAAGGGACCTGAAATGACCCCTGTG
5451 CCTTATTGAACTAACCAATCAGTTCGTTCTCGCTTCTGTTCGCGCCT
5501 TCTGCTCCCCGAGCTCAATAAAAGAGGCCACACCCCTCACTGGGGCGC
5551 CAGTCCTCCGATTGACTGAGTCGCCGGTACCCGTGTATCCAATAAAC
5601 CTCTTGCAAGTGCATCCGACTTGTGGTCTCGCTGTTCTGGAGGGTCT

Figure 14c

5651 CCTCTGAGTGATTGACTACCCGTCAGCGGGGTCTTCATT

1 - 2053	Bovine/Human Alpha-lactalbumin 5' flanking region
2093 - 2336	Double mutated PPE sequence
2403 - 2459	Bovine alpha-lactalbumin signal peptide coding region
2460 - 3137	Yersenia pestis heavy chain Fab gene coding region
3167 - 3742	EMCV IRES
3743 - 3799	Bovine alpha-lactalbumin signal peptide coding region
3800 - 4441	Yersenia pestis light chain Fab gene coding region
4461 - 5052	WPRE sequence
5098 - 5691	Moloney murine leukemia virus 3' LTR

Figure 15
SEQ ID NO:12
IRES-Casein Signal Peptide Sequence

1 GGAATTGCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCG
51 CTTGGAATAAGGCCGGTGTGCGTTGTCTATATGTTATTTCCACCATAT
101 TGCCGTCTTTGGCAATGTGAGGGCCCGAAACCTGGCCCTGTCTTCTTG
151 ACGAGCATTCTAGGGGTCTTCCCCTCTGCCAAAGGAATGCAAGGTCT
201 GTTGAATGTCGTGAAGGAAGCAGTTCTCTGGAAGCTTCTTGAAGACAAA
251 CAAAGTCTGTAGCGACCCCTTGCAAGGAGCGGAACCCCCCACCTGGCGAC
301 AGGTGCCTCTGGCCAAAAGCCACGTGTATAAGATAACACCTGCAAAGGC
351 GGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGAAAGAGTCA
401 AATGGCTCTCTCAAGCGTATTCAACAAAGGGGCTGAAGGATGCCAGAAG
451 GTACCCCATTGTATGGGATCTGATCTGGGCCTCGGTGCACATGTTTAC
501 ATGTGTTAGTCGAGGTTAAAAAAACGTCTAGGCCCGAACCACGGGG
551 ACGTGGTTTCTTGGATGATAATATGGCCTTGTCTCATCCT
601 TACCTGTCTTGTGGCTGTTGCTTGGCGGCCATGGGATATCTAGATC
651 TCGAGCTCGCAAAGCTT

1 - 583
584 - 628
629 - 668

IRES
Modified bovine alpha-S1 casein signal peptide coding region
Multiple cloning site

Figure 16a

SEQ ID NO: 13

LNBOTDC Vector

1 TTTGAAAGACCCACCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT
51 TGCAAGGCATGAAAAATACATAACTGAGAATAGAAAAGTTCAAGATCAAG
101 GTCAGGAACAAGAACAGCTGAATACCAAACAGGATATCTGTGGAAGC
151 GGTCCTGCCCGGCTCACGGCCAAGAACAGATGAGACAGCTGAGTGATG
201 GGCCAAACAGGATATCTGTGGAAGCAGTCCCTGCCCGGCTCGGGGCCA
251 AGAACAGATGGTCCCAGATGCGGTCCAGCCCTCAGCAGTTCTAGTGAA
301 TCATCAGATGTTCCAGGGTCCCCAAGGACCTGAAAATGACCCCTGTACC
351 TTATTTGAACTAACAAATCAGTCGCTTCTCGCTCTGTTCGCGCGCTTC
401 CGCTCTCCGAGCTCAATAAAAGAGCCACAAACCCCTCACTCGCGCGCCA
451 GTCTCCGATAGACTGCGTCGCCGGTACCCGTATTCCCAATAAGCCT
501 CTTGCTGTTGCATCGAACATGTGGTCTCGCTGTTCTGGGAGGGCTC
551 CTCTGAGTGATTGACTACCCACGACGGGGCTTTCATTGGGGGCTCGT
601 CGGGGATTGGAGACCCCTGCCAGGGACCACCGACCCACCGGGGAGG
651 TAAGCTGCCAGCACTTATCTGTGCTGTCCGATTGTCTAGTGTCTATG
701 TTTGATGTTATGCCGCTGGCTGTACTAGTTAGCTAACTAGCTCTGTAT
751 CTGGCAGGCCCTGGTGGAACTGACGAGTTCTGAAACACCCGGCGCAACC
801 CTGGGAGACCTCCAGGGATTGGGGCCGTTTGTGGCCGACCTGA
851 GGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGTTCTGGT
901 AGGAGACGAGAACCTAAAACAGTCCCGCTCCGCTGAATTGGCTTT
951 CGGTTTGGAAACCGAAGCCGCGCTTGTCTGCTGAGCGCTGCAGCATC
1001 GTTCTGTGTTGCTCTGTGACTGTGTTCTGATTGTCTGAAAATTAA
1051 GGGCCAGACTGTTACCACTCCCTTAAGTTGACCTTAGGTCACTGGAAAG
1101 ATGTCGAGCGATCGCTACAACCACTCGGTAGATGTCAGGAAGAGACGT
1151 TGGGTTACCTCTGCTCTGCAAGATGCCAACCTTAACGTCGGATGGCC
1201 GCGAGACGGCACCTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGG
1251 TCTTTCACCTGGCCCGCATGGACACCCAGACCGAGGCTCCATCGTG
1301 ACCTGGGAAGCCTGGCTTGACCCCCCTCCCTGGGTCAGGCCCTTGT
1351 ACACCCCTAACGCCCTCCGCTTCTCCATCCGCCGCTCTCTCCCC
1401 TTGAACCTCTCGTTGCAACCCGCCCTCGATCTCCCTTATCCAGGCC
1451 ACTCCCTCTCAGGCGCCGAATTCCGATCTGATCAAGAGACAGGATGAG
1501 GATCGTTTCGATGATTGAAACAGATGGATTGACGCGCAGGTTCTCCGCC
1551 GCTTGGGTGGAGAGGCTATTGGCTATGACTGGCACAACAGACAATCGG
1601 CTGCTCTGATGCCGCGTGTTCGGCTGTCAGGGCAGGGGCCGGTT
1651 TTTTGTCAGGACCGACCTGTCGGTGCCTGAATGAAGTGCAGGACGAG
1701 GCAGCGGGCTATCGTGGCTGCCACGACGGGCGTTCCCTGCGCAGCTGT
1751 GCTCGACGTTGTCAGTAAGCGGGAGGGACTGGCTGATTTGGCGAAG
1801 TGCCGGGGCAGGATCTCTGTCATCTCACCTTGTCTGCCAGAAAGTA
1851 TCCATCATGGCTGATGCAATGCGGGCGCTGCACTACGCTTGTACGGCTAC
1901 CTGCCATTGCGGCAACCAAGCGAACATCGCATCGAGCGAGCACGTACTC
1951 GGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAG
2001 GGGCTCGGCCAGCGAAGTGTGCCAGGCTCAAGGCGCCATGCCGA
2051 CGCGAGGATCTCGTCGACCCATGGCGATGCCGCTTGGCAATATCA
2101 TGGTGGAAAATGGCGCTTTCTGGATTCTGATCGACTGTGCCGGCTGGG
2151 GTGGCGGACCGTATCAGGACATAGCGTTGGCTACCGTGATATTGCTGA
2201 AGAGCTGGCGGCGAATGGGCTGACCGCTCCCTGTGCTTACGGTATCG
2251 CCCTCCCGATTCCGACCCGATCCGCTTCTATCGCTTCTGACGAGTTC
2301 TTCTGAGCGGACTCTGGGTTGCAATGACCGACCAAGCGACGCCAAC
2351 CTGCCATACGAGATTCGATCCACCGCCGCTTCTATGAAAGGTTGGG
2401 CTTCGGAATGTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGG
2451 ATCTCATGCTGGAGTTCTCGCCACCCGGCTGATCCCTCGCGAGT
2501 TGGTTCACTGCTGCCAGGCTGACGACCTCGCGGAGTCTACCGGCA
2551 GTGCAAATCCGTCGGCATCCAGGAAACCCAGCAGCGGCTATCCGCGCATCC
2601 ATGCCCCCGAACCTGCAAGGAGTGGGGAGGCACGATGGCGCTTGGTC
2651 GCGGATCCGCCATTACCCATATTATTCATTGGTTATATAGCATAAAATCA
2701 ATATTGGCTATTGGCCATTGCATACGTTGATCCATATCATAATATGTAC
2751 ATTTATATTGGCTCATGCTAACATTACCGCCATGTTGACATTGATTATT

Figure 16b

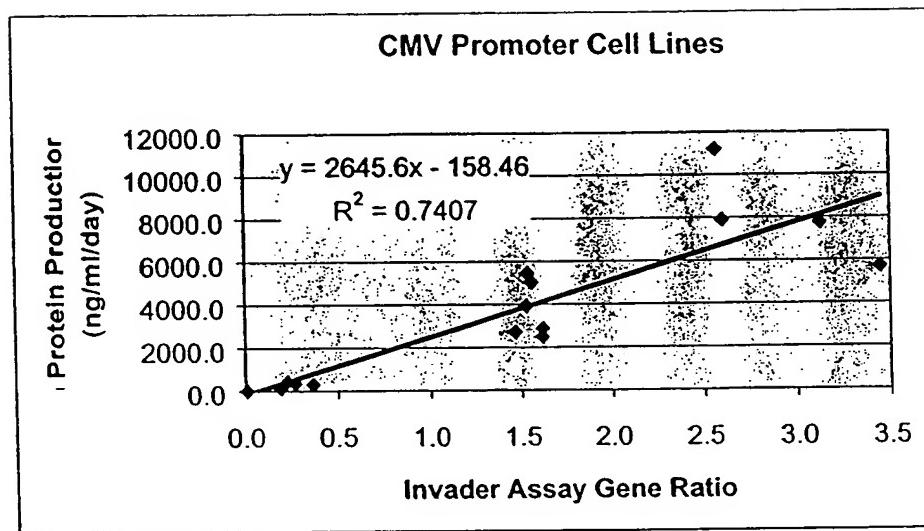
2801 GACTAGTTATAATAGTAATCAATTACGGGTCAATTAGTCATAGCCCCAT
2851 ATATGGAGTTCCCGGTTACATAACTTACGGTAAATGGCCCGCTGGCTGA
2901 CCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCAT
2951 AGTAAACGCCAATAGGGACTTCCATTGACGTCAATGGGTGGAGTATTAC
3001 GGTAAAATGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACG
3051 CCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCA
3101 GTACATGACCTTATGGGACTTCCACTTGGCAGTACATCTACGTATTAG
3151 TCATCGCTATTACCATGGTATGCGGTTTGGCAGTACATCAATGGCGT
3201 GGATAGCGGTTGACTCACGGGATTCCAAGTCTCCACCCATTGACGT
3251 CAATGGGAGTTGTTTGGCACC AAAAATCAACGGGACTTCCAAAATGTC
3301 GTAACAACCTCCGCCCCATTGACGCAAATGGCGGTAGGCATGTACGGTGG
3351 GAGGTCTATATAAGCAGAGCTCGTTAGTGAACCGTCAGATCGCCTGGAG
3401 ACGCCATCCACGCTGTTTGACCTCCATAGAACAGACACCGGGACCGATCCA
3451 GCCTCCGGGCCCAAGCTCTCGACGGATCCCGGGATTCAAGGCCATC
3501 GATCCCAGGCCACCATGGAATGGAGCTGGTCTTCTCTTCTGT
3551 AGTAACATCAGGTGTCACCTCCGACATCCAGATGACCCAGTCTCCAGCCT
3601 CCCTATCTGCATCTGTTGGAGAAACTGTCACTATCACATGTCGAGCAAGT
3651 GGGAAATTCAAAATTATTAGCATGGTATCAGCAGAAACAGGGAAATC
3701 TCCTCAGCTCTGGCTATAATGCAAAAACCTTACAGATGGTGTGCCAT
3751 CAAGGTTCACTGGCAGTGGATCAGGAACACAATTCTCTCAAGATCAAC
3801 AGCCTGCAGCCTGAAGATTGGGAGTTATTACTGTCAACATTGGAG
3851 TACTCCGTGGACGTTCGGTGGAGGCACCAAGCTGAAATCAAACGGGCTG
3901 ATGCTGCACCAACTGTATCCATCTTCCCACCATCAGTGAGCAGTTAAC
3951 TCTGGAGGTGCTCACTCCTGTGCTTCTGAACAACACTTCAACCCAAAGA
4001 CATCAATGTCAGTGGAAAGATTGATGGCAGTGAACGACAAAAATGGCGTCC
4051 TGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGC
4101 AGCACCCCTCACATTGACCAAGGACGAGTATGAACGACATAACAGCTATAAC
4151 CTGTGAGGCCACTCACAAGACATCAACTCACCCATTGTCAGAGCTTCA
4201 ACAGGAATGAGTGTGAAAGCATCGATTCCCTGAATTGCCCTCTCC
4251 CTCCCCCCCCCTAAGTTACTGGCGAAGCCGCTTGGATAAAGGCCGT
4301 GTGCGTTGCTATATGTTATTCCACCATATTGCGCTTCTGACGAGCATTCTAGGG
4351 GTGAGGGCCCAAACCTGGCCCTGCTTCTGACGAGCATTCTAGGG
4401 TCTTCCCCCTCGCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGG
4451 AACAGATTCTCTGGAGCTTCTTGAAGACAACACAGTCTGTAGCGACC
4501 CTTTGAGGCAGCGAACCCCCCACCTGGGACAGGTGCTCTGGGCCA
4551 AAAGCCACGTGTATAAGATAACACCTGCAAAGGGGGACAACCCAGTGCC
4601 ACGGTGTGAGTTGGATAGTTGTGAAAGAGTCAAATGGCTCTCTCAAGC
4651 GTATTCAACAAGGGCTGAAGGATGCCAGAAGGTACCCATTGTATGG
4701 ATCTGATCTGGGCTCTGGTCACATGTTACATGTGTTAGTCGAGGT
4751 TAAAAAAACGCTTAGGCCCCCGAACACGGGGACGTGGTTTCTTTGA
4801 AAAACACGATGATAATATGGCCTCCTTGTCTCTGCTCTGGTAGGCA
4851 TCCTATTCCATGCCACCCAGGCCAGGTTCACTTCAGCAGTCTGGGGCA
4901 GAGCTGTGAAGCCAGGGCCTCACTCAAGTTGTCTGCACAGCTCTGG
4951 CTTCAACATTAAAGACACCTTATGCACTGGGTGAAGCAGAGGCCCTGAAC
5001 AGGGCTGGAGTGGATTGAAAGGATTGATCCCTGGAATGGGAAACTGAA
5051 TATGACCGAAGTCCAGGGCAAGGCAACTATAACAGCAGACACATCCCTC
5101 CAAACAGTCACCTGCACTCAGCAGCTGACATCTGAGGACACTGCC
5151 TCTATTACTGTGCTAGTGGAGGGAACTGGGGTTTCTTACTGGGGCAA
5201 GGGACTCTGGTCACTGTCTGCACTGGGAAACAGCACCCCCATCTGCTA
5251 TCCACTGGCCCTGGATCTGCTGCCAAACTAACTCCATGGTGAACCTGG
5301 GATGCCCTGGTCAAGGGTATTCTGAGCCAGTGAAGTGAACCTGGAAC
5351 TCTGGATCCCTGTCCAGGGTGTGCAACCTTCCAGCTGTCTGCAGTC
5401 TGACCTCTACACTCTGAGCAGCTCACTGACTGTCCCCCTCCAGCACCTGG
5451 CCAGCGAGACCGTCACCTGCAACGTTGCCACCCGGCAGCAGCACCAAG
5501 GTGGACAAGAAAATTGTGCCCCAGGGATTGTAAGTGGAGGTGGAGGTAG
5551 CCACCATCACCATCACCAATTAACTAGGTTAAAGCAGGCGTCAGATCTA
5601 GGCCCTCTAGGTGACATCGATAAAATAAAAGATTATTAGTCTCCAG
5651 AAAAAGGGGGAAATGAAAGACCCACCTGTAGGTTGGCAAGCTAGCTTA
5701 AGTAACGCCATTGCAAGGATGGAAAAATACATAACTGAGAATAGAGA
5751 AGTCAGATCAAGCTCAAGAACAGATGGAACAGCTGAATATGGCCAAAC
5801 AGGATATCTGTGGAAGCAGTTCTGCCCGGCTCAGGGCCAAGAACAGA
5851 TGGAACAGCTGAATATGGCCAAACAGGATATCTGTGGAAGCAGTTCT

Figure 16c

5901 GCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGCCAGCCCT
5951 CAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGCCCCAAGGACCT
6001 GAAATGACCGCTGTGCCTTATTGAACCAACCAATCAGTCGCTTCTCGCT
6051 TCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCC
6101 CTCACTCGGGGCCAGTCCTCGATTGACTGAGTCGCCGGTACCCGT
6151 GTATCCAATAAACCTCTTGAGTTGCATCCGACTTGTGGTCTCGCTGTT
6201 CCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCGTCAGCGGGGTCTT
TCATT

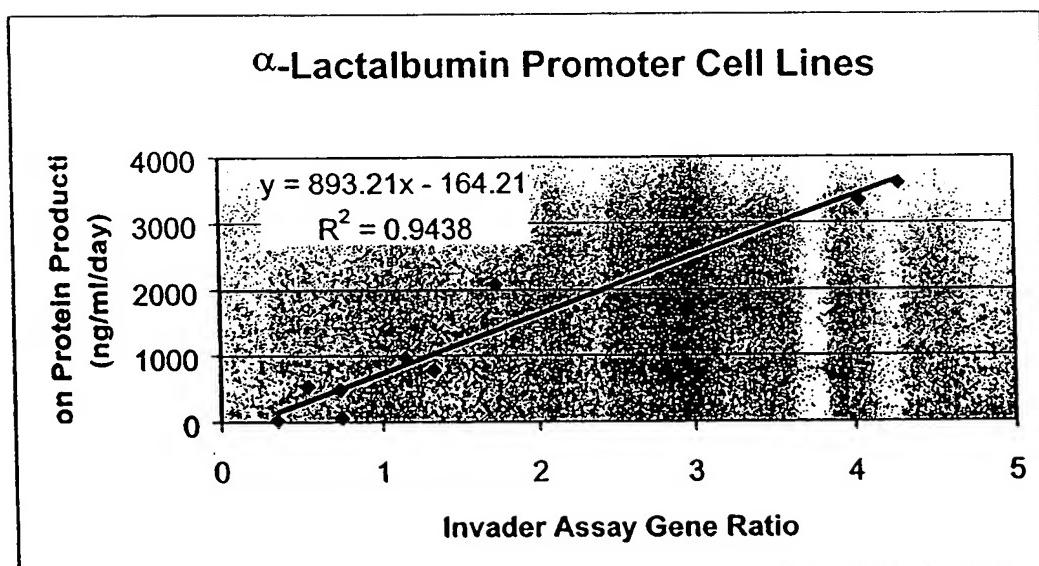
Moloney Murine Sarcoma Virus 5' LTR	1 - 589
Moloney Murine Leukemia Virus Extended Packaging Region	659 - 1468
Neomycin Resistance Gene	1512 - 2306
CMV Promoter	2656 - 3473
cc49 Signal Peptide Coding Region	3516 - 3572
Bot Fab 5 Light Chain	3573 - 4217
EMCV IRES (Clonetech)	4235 - 4816
Modified Bovine α -LA Signal Peptide Coding Region	4817 - 4873
Bot Fab 5 Heavy Chain	4874 - 5572
Moloney Murine Leukemia Virus 3' LTR	5662 - 6255

Figure 17. CMV construct containing cell lines.



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Figure 18: α -Lactalbumin construct containing cell lines



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Figure 19a
SEQ ID NO: 34
LNBOTDC Vector

1 GAATTAATTCATACCAGATCACCGAAAATGTCTCCAAATGTGTCCCCC
51 TCACACTCCCAAATTGCGGGCTCTGCCTTCTAGACCACTCTACCCCTAT
101 TCCCCACACTCACCGGAGCCAAGGCCGGCCCTCCGTTCTTGCTTT
151 TGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTG
201 CAAGGCATGGAAAAAATACATAACTGAGAAATAGAAAAGTTCAAGATCAAGGT
251 CAGGAACAAGAACAGCTGAATACCAAAACAGGATATCTGTGTAAGCGG
301 TTCTGCCCCGGCTCAGGCCAAGAACAGATGAGACAGCTGAGTGTAGGG
351 CAAACAGGATATCTGTGTAAGCAGTCTGCCGGCTGGGGCAAG
401 AACAGATGGTCCCAGATCGCGTCCAGCCCTCAGCAGTTCTAGTGAATC
451 ATCAGATGTTCCAGGTGCCCCAAGGACCTGAAAATGACCTGTACCTT
501 ATTGAACTAACCAATCAGTCGCTTCTCGCTTCTGTCGCGCTTCCG
551 CTCTCGAGCTCAATAAAAGGCCACAACCCCTCACTCGGCGCCAGT
601 CTTCGATAGACTCGCTGCCGGTACCCGTATCCAAATAAGCCCT
651 TGCTGTTGCAATCGTGGTCTCGCTGTTCTGGGAGGGTCTCCT
701 CTGAGTGAATTGACTACCCACGACGGGGTCTTCATTGGGGCTCGTCC
751 GGGATTGGAGACCCCTGCCAGGGACCACCGACCCACCCACGGGAGGTA
801 AGCTGGCCAGCAACTTATCTGTGTCGCTGCGATTGTCTAGTGTCTATGTT
851 TGATGTTATGCGCCTGCGTCTGTAAGTTAGCTAACTAGCTGTATCT
901 GCGGGACCCGTGGTGAACGTACGAGTTCTGAACACCCGGCCGAACCCCT
951 GGGAGACGTCCCAGGGACTTGGGGGGCTTTTGTCGGCCGACCTGAGG
1001 AAGGGAGTCGATGTTGAATCCGACCCCGTCAGGATATGTGGTCTGGTAG
1051 GAGACGAGAACCTAAACAGTTCGGCCTCCGTCGATTTTGCTTTCG
1101 GTTGGAAACCGAAGCCGCGTCTGCTGAGCAGCGCTGAGCATCGT
1151 TCTGTTGCTCTGCTGACTGTGTTCTGATTTGCTGAAAATTAGG
1201 GCCAGACTGTACCAACTCCCTTAAGTTGACCTTAGTCAGTGAAAGAT
1251 GTCGAGCGGATCGCTCACACCAGTCGGTAGATGTCAGAACAGAGACGTTG
1301 GTTACCTCTGCTCTGAGAATGGCAACCTTAACCTCGGATGGCCGC
1351 GAGACGGCACCTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTC
1401 TTTTACCTGGCCCGCATGGACACCCAGACGGCTCCCTACATCGTGC
1451 CTGGGAAGCCTTGGCTTGACCCCCCTCCCTGGGTCAGCCCTTTGTA
1501 ACCCTAAGCCTCCGCTCCTCTCCATCCGCCCCGTCCTCCCCCT
1551 GAACTCCTCGTTGACCCCGCCTCGATCCTCCCTTATCCAGCCCTCAC
1601 TCTTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAGGG
1651 AGCTTGTATATCCATTTCGGATCTGATCAGCACGTGTTGACAATTATC
1701 ATCGGCATAGTATATCGGCATAGTATAATACGCAAGGTGAGGAACCTAA
1751 CCATGGCAAGCCTTGTCTCAAGAAGAATCCACCCCTCATTGAAAGAGCA
1801 ACGGCTACAATCACAGCACCCATCTGAGACTACAGCGTCGCCAG
1851 CGCAGCTCTCTAGGCGCCGCACTCTCACTGGTGTCAATGTATATC
1901 ATTAACTGGGGACCTTGTGAGAACCTCGTGGTGTGGCACTGCTGCT
1951 GCTGCGGCAGCTGGCAACCTGACTTGATCTGTCGCGATCGGAAATGAGAA
2001 CAGGGGCATCTTGAGCCCTGCGGACGGTGTGACAGGTGCTCTCGATC
2051 TGCATCTGGGATCAAAGCGATAGTGAAGGACAGTGTGAGACAGCCGACG
2101 GCAGTTGGGATTCTGAAATTGCTGCCCTCGGTTATGTGTTGGAGGGTA
2151 AGCACCTCGTGGCCAGGGAGCAGGACTGACACGTCGCTACGAGATTGAT
2201 TCCACCGCCCTCTATGAAAGGTTGGCTTCCGAATCGTTTCCGGGA
2251 CGCCGGCTGGATGATCTCCAGCGGGGGATCTCATGCTGGAGTTCTCG
2301 CCCACCCAACTTGTATTGCAAGCTATAATGGTTACAAATAAGCAAT
2351 AGCATCACAAATTCAAAATAAGCATTTCACTGCATTCTAGTTG
2401 TGGTTTGTCAAACCTCATCAATGTATCTTATCATGTCGTCAGGTTGGT
2451 TCAGCTGTCGCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
2501 AAATCCGTCCGGCATCCAGGAAACCGAGCAGCGCTATCCGCGCATCCATGC
2551 CCCCGAAGTCAGGAGTGGGGAGGCACGATGGCCCTTGGTCAGGGCG
2601 ATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAAATCAATAT
2651 TGGCTATTGGCCATTGCACTACGTTGATCCATATCATAATATGTACATT
2701 ATATTGGCTCATGTCCAACATTACGGCCATGTGACATTGATTATTGACT
2751 AGTTATTAAATAGTAATCAATTACGGGTCAATTAGTCATAGCCCATATAT
2801 GGAGTTCCGGTACATAACTTACGGTAATTGGCCCGCTGGCTGACCGC
2851 CCAACGACCCCCGGCCATTGACGTCAATAATGACGTATGTTCCCATAGTA

Figure 19b

2901 ACGCCAATAGGGACTTCCATTGACGTCAATGGGTGGAGTATTTACGGTA
2951 AACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCC
3001 CTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCCAAGTAC
3051 ATGACCTTATGGGACTTCTACTTGGCAGTACATCTACGTATTAGTCAT
3101 CGCTATTACCATGGTATGCAGGTTTGGCAGTACATCAATGGCGTGGAT
3151 AGCGGTTTGAACCTCACGGGATTCCAAGTCTCCACCCATTGACGTCAAT
3201 GGGAGTTTGTGTTGGCACCRAAATCAACGGGACTTCCAATAATGTCGTA
3251 CAACTCCGCCCCATTGACGCAAATGGCGGTAGGCATGTACGGTGGGAGG
3301 TCTATATAAGCAGAGCTGTTAGTGAACCGTCAGATGCCCTGGAGACGC
3351 CATCCACGCTGTTTGACCTCCATAGAACAGACCCGGGACCGATCCAGCCT
3401 CCGCGGCCCAAGCTCTCGAGTTAACAGATCTAGGCTGGCACGACAGGT
3451 TTCCCGACTGAAAAGCGGGCAGTGAACGCAATTAAATGTGAGTTAG
3501 CTCACTCATTAGGCACCCCAGGCTTACACTTTATGCTTCCGGCTCGTAT
3551 GTTGTGTGAAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATG
3601 ACCATGATTACGCCAAGCTGGCTGCAGGTCAGGATCCACTAGTAACG
3651 GCCGCCAGTGTGCTGGAATTCAACCATGGGGCAACCCGGGAAACGGCAGCG
3701 CTTCTTGCTGGCACCCATGGAAAGCCATGCCGGGACACGACGTCACGC
3751 AGCAAAGGGACGGTGTGGTGGTGGCATGGGATCGTCATGTCATCTC
3801 ATCGTCTGGCCATCGTGTGGCAATGTGCTGGTCATCACAGCATTG
3851 CAAGTCGAGCGCTGCAGACGGTCACCAACTACTTCATCACAAGCTTG
3901 CCTGTGCTGATCTGGTCATGGGCTAGCAGTGGTGCCTTGGGCC
3951 CATATTCTCATGAAAATGTGACTTTGGCAACTCTGGTGCAGGTTCTG
4001 GACTTCATTGATGTGCTGCGTCACGGCATCGATTGAGAACCTGTGCG
4051 TGATCGCAGTGCACCGCTACTTGCCATTACTAGTCCTTCAGTACCAAG
4101 AGCCTGCTGACCAAGAATAAGGCCGGTGATCATTCTGATGGTGTGGAT
4151 TGTGTCAGGCCCTACCTCCTTGCCTTCAGATGCACTGGTACAGGG
4201 CCACCCACCAGGAAGCCATCAACTGCTATGCCATTGCTTCATGTC
4251 TTCTTCACGAACCAAGCTATGCCATTGCTTCATGTC
4301 CGTCCCCCTGGTATCGGTCTTCGTTACTCCAGGGTCTTCAGGAGG
4351 CCAAAGGCAGCTCCAGAAGATTGACAAATCTGAGGGCCGCTCCATGTC
4401 CAGAACCTTAGCCAGGTGGAGCAGGATGGGGCGACGGGGCATGGACTCCG
4451 CAGATCTTCAAGTCTGTTGAAGGGAGCACAAAGCCCTCAAGACGTTAG
4501 GCATCATCATGGGCACTTCAACCTCTGCTGGCTGCCCTTCTCATCGTT
4551 AACATTGTGATGTGATCAGGATAACCTCATCCGTAAAGGAAGTTACAT
4601 CCTCTAAATTGGATAGGCTATGTCATTCTGGTTCAATCCCTTATCT
4651 ACTGCCGGAGCCCAGATTTCAGGATTGCCCTCCAGGAGCTCTGTGCC
4701 CGCAGGTCTCTTGAGGCCTATGCCATTGCTACTCCAGCAACGGCAA
4751 CACAGGGGAGCAGAGTGGATATCACGTGGAACAGGGAGAAAGAAAATAAAC
4801 TGCTGTGAGAGCCTCCAGGACCGGAAGACTTGTGGGCCATCAAGGT
4851 ACTGTGCTTAGCGATAACATTGATTGACAAGGGAGGAATTGTA
4901 TGACTCACTGCTCTCGAGAATCGAGGGCGGCACCACCATCATCACCACG
4951 TCGACCCCGGGACTACAAGGATGACGATGACAAGTAAGCTTATCCATC
5001 ACACGGCCGCGCTCGACATGCATCTAGCGGGCGCTCGAGGGCGGCAA
5051 GGCGGATCCCCGGAAATTGCCCTCTCCCTCCCCCCCCCTAACGTTA
5101 CTGGCGAAGCCGCTTGAATAAGGCCGGTGTGGTTGTCTATATGT
5151 TTTCCACCATATTGCCCTTGGCAATGTGAGGGGGGGAAACCTGG
5201 CCTGTCTTGTGACGAGCATTCCTAGGGTCTTCCCTCTGCC
5251 GAATGCAAGGCTCTGGATGTGCTGAAGGAAGCAGTCCCTGGAAGCT
5301 TCTTGAAGACAAACAAAGCTGTAGCGACCCCTTGCGAGCAGCGGAACCC
5351 CCCACCTGGCGACAGGTGCCTGCCGGCAAAGGCCACGTGTATAAGATA
5401 CACCTGCAAAGGGCACAACCCAGTGCACGGTTGTGAGTTGGATAGTT
5451 GTGGAAGAGTCAAATGGCTCTCCATCAAGCTTCAACAAGGGGCTGAA
5501 GGATGCCCAAGAAGGTACCCATTGTATGGGATCTGATCTGGGCC
5551 GCACATGCTTACATGTGTTAGTCGAGGTTAAAAAAACGTCAGGCC
5601 CGAACACCAGGGGACGTGGTTTCTTGGAAAGAACACGATGATAATATGG
5651 CCTCTTGTCTCTGCTCTGGTAGGCATCCATTCCATGCCACCCAG
5701 CGCGAGCTCACCCAGTCTCCAGACTCCCTGGCTGTGTCTGGCGAGAG
5751 GGCCACCATCAACTGCAAGTCCAGCCAGAGTGTGTTGTACAGCTCCA
5801 ATAAGAACTTGTGGTATCAGCAGAAACCCAGGACAGCCTCTAAC
5851 CTGCTCATTACTGGGATCTACCCGGGAATCCGGGGTCCCTGACCGATT
5901 CAGTGGCAGGGGTCTGGGACAGATTCACTCTCACCATCAGCAGCTGC
5951 AGGCTGAAGATGTGGCAGTTATTACTGTCAAGCAATATTAGTACTCAG

Figure 19c

6001 ACCTTCGGCCAAGGGACCAAGGTGAAATCAAACGAACGTGGCTGCACC
6051 ATCTGTCTTCATCTTCCCCTCATCTGATGAGCAGTTGAAATCTGGAACGTG
6101 CCTCTGTTGTGCGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTA
6151 CAGTGGAAAGGTGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGT
6201 CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGA
6251 CGCTGAGCAAAGCAGACTACGAGAAAACACAAACTCTACGGCTCCGGAAGTC
6301 ACCCATCAGGGCCTGAGATCGCCCGTCACAAAGAGCTTCACAAGGGGAG
6351 AGTGTAGTTCTAGATAATTAAATTAGGAGGAGATCTGAGCTCGCGAAAC
6401 CTTGGCACTGGCGTCGTTTACAACGTCGTGACTGGGAAACCCCTGGCG
6451 TTACCCAACCTTAATCGCCTTGCAAGCACATCCCCCTTCGCCAGCCTCTA
6501 GGTGACATCGATAAAAATAAAAGATTATTTAGTCTCCAGAAAAGGGG
6551 GGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCC
6601 ATTTTGAAGGCATGGAAAAAATACATAACTGAGAATAGAGAACGTTAGAT
6651 CAAGGTAGGGACAGATGGAACAGCTGAATATGGCCAAACAGGATATCT
6701 GTGTTAAGCAGTCTGCGCCGGCTCAGGGCCAAGAACAGATGGAACAGC
6751 TGAATATGGGCAACAGGATATCTGTTGTAAGCAGTTCTGCCCCGGCT
6801 CAGGGCAAGAACAGATGGTCCCAGATGCGGTCCAGGCCCTCAGCAGTT
6851 CTAGAGAACCATCAGATGTTCCAGGGTGCCCAAGGACCTGAAATGACC
6901 CTGCGCTTATTGAACTAACCAATCAGTCGCTTCTCGCTTCTGTTCGC
6951 GCGCTCTGCTCCCCGAGCTCAATAAAAGAGCCACAACCCCTACTCGG
7001 GGGCCAGTCCTCGATTGACTGAGTCGCCCGGTACCCGTGTATCCAAT
7051 AAACCCCTCTGCACTGCGATCCGACTTGTGGTCTCGCTGTTCTGGGAG
7101 GGTCTCTCTGAGTGTGACTACCCGTCAAGCGGGGTCTTCAATTGGG
7151 GGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGACCACGCCACAC
7201 CGGGAGGTAAGCTGGCTGCCCTCGCGCTTCGGTGATGACGGTAAAACC
7251 TCTGACACATGCAGCTCCCGAGACGGTCACAGCTGTCTGTAAGCGGAT
7301 GCCGGGAGCAGACAAGCCCGTCAGGGCGCTCAGCGGGGTGTGGCGGGTG
7351 TCGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTG
7401 GCTTAACATAGCGGCATCAGAGCAGATTGACTGAGAGTGCACCATATGC
7451 GGTGTGAAATACCGCACAGATGCGTAAGGGAGAAAATACCGCATCAGCGC
7501 TCTTCGGCTTCTCGCTACTGACTCGCTCGCTCGGTCTCGCTGCG
7551 GCGAGCGGTATCAGCTACTCAAAGCGGTAAATACGGTTATCCACAGAAAT
7601 CAGGGGATAACCGCAGGAAAGAACATGTGAGCAGAACAGGCCAGAAAAGGC
7651 AGGAACCGTAAAAGGCCGCGTTGCTGGCCTTTCCATAGGCTCCGCC
7701 CCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCAAACCC
7751 CGACAGGACTATAAAGATACCAGCGTTTCCCGTGGAAAGCTCCCTCGT
7801 CGCTCTCTGTTCCGACCCCTGCCGCTTACCGGATACCTGTCGCCCTTCT
7851 CCCTCGGGAAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGTATCTCA
7901 GTCCGGTGTAGGTCGCTCCAGCTGGCTTATCCGGTAACTATCGTCTGAGTCAA
7951 GTTCAGCCCGACCGCTGCCCTTATCCGGTAACTATCGTCTGAGTCAA
8001 CCCGGAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGA
8051 TTAGCAGAGCAGGGTATGTAAGCGGTGCTACAGAGTTCTGAGTGGGG
8101 CCTAACTACGGCTACACTAGAAGGCAGTATTGGTATCTGCGCTCTGCT
8151 GAAGCCAGTACCTTCGAAAAAGAGTTGGTAGCTCTGATCCGGCAAAC
8201 AAACCCACCGCTGGTAGCGGTGGTTTTTGTGAGTCTACGGGT
8251 CGCAGAAAAAAAGGATCTCAAGAAGATCCTTGTATCTACGGGT
8301 TGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTGGTATGAGAT
8351 TATCAAAAAGGATCTCACCTAGATCCTTTAAATTAAAAATGAAGTTT
8401 AAATCAATCTAAAGTATATGAGTAAACTTGGTCTGACAGTTACCAATG
8451 CTTAATCAGTGAGGCACCTATCTCAGCGATCTGCTATTCTGTCATCA
8501 TAGTTGCTGACTCCCGCTGTAGATAACTACGATACGGGAGGGCTTA
8551 CCATCTGGCCCCAGTGTGCAATGATACCGCAGGCCACCGTCACCGGC
8601 TCCAGGTTTACGCAATAAACAGCCAGCCGAAGGGCCAGCGCAGAA
8651 GTGGTCTGCAACTTTATCGCCCTCATCCAGTCTATTAAATTGTCGCC
8701 GAAGCTAGAGTAAGTAGTTGCCAGTTAATAGTTGCGAACGTTGTC
8751 CATTGCTGCAGGCATGTGGTGTACGCTCGTCGTTGGTATGCCCTCAT
8801 TCAGCTCCGGTTCCCAACGATCAAGGCAGTTACATGATCCCCCATGTTG
8851 TGCAAAAAGCGGTTAGCTCTCGGTCTCCGATCGTTGTCAGAAAGTAA
8901 GTTGGCCGAGTGTATCACTCATGGTTATGGCAGCAGTGCATAATTCTC
8951 TTACTGTCTGAGAATAGTGTATGCGGCCACCGAGTTGCTCTGCC
9001 ACCAAGTCATTCTGAGAATAGTGTATGCGGCCACATAGCAGAACTTTAAAAGTGC
9051 GGCCTCAACACGGATAATACCGGCCACATAGCAGAACTTTAAAAGTGC

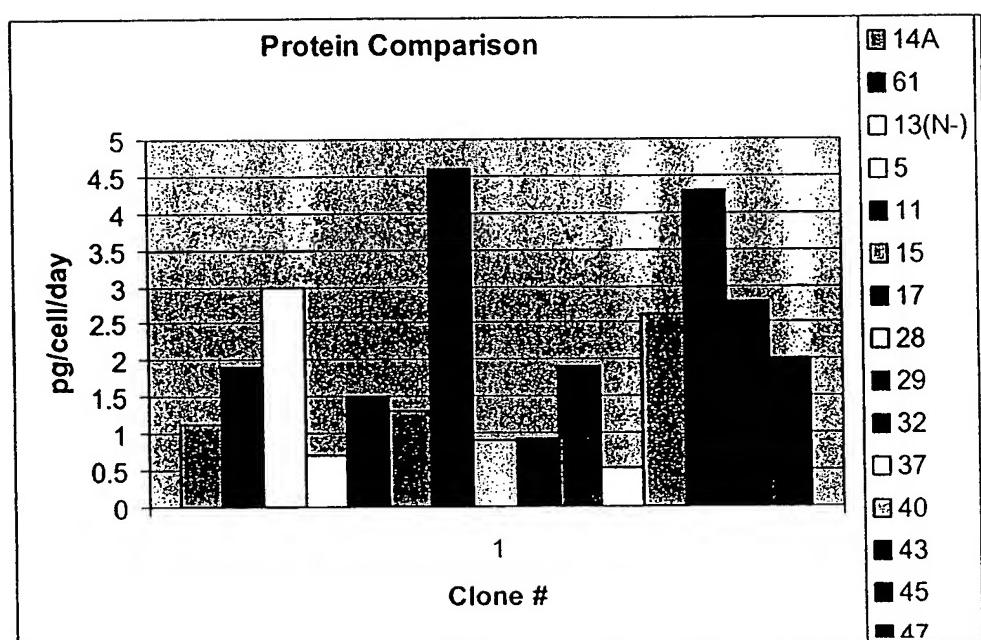
Figure 19d

9101 TCATCATTGGAAAACGTTCTCGGGGCAAAACTCTCAAGGATCTTACCG
9151 CTGTTGAGATCCAGTCGATGTAACCCACTCGTCACCCAACTGATCTC
9201 AGCATCTTTACTTCACCAGCGTTCTGGGTGAGCAAAAACAGGAAGGC
9251 AAAATGCCGCAAAAAGGGAATAAGGGCGACACGAAATGTTGAATACTC
9301 ATACTCTTCCTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCT
9351 CATGAGCGGATACATATTGAATGTATTAGAAAAATAACAAATAGGGG
9401 TTCCGCGCACATTCGGGAAAAGTGCCACCTGACGTCTAAGAAACCATT
9451 ATTATCATGACATTAACCTATAAAAATAGGCGTATCAGGAGGCCCTTCG
1. TCTTCAGAAAT

Features:

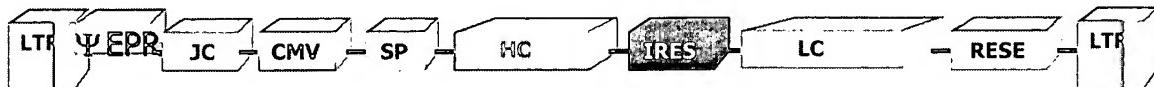
149-737 Moloney murine sarcoma virus 5' LTR
807-1616 Extended Packaging Region
1680-1735 EM7 promoter (bacteriophage T7 promoter)
1754-2151 Blasticidin resistance gene coding sequence
2310-2440 SV40 poly A signal and site
2603-3420 CMV IE promoter
3675-4988 G-protein-coupled receptor (GPCR)
5071-5646 IRES
5647-5703 Bovine α -lactalbumin signal peptide
5704-6372 'humanized' antibody light chain
6553-7146 MoMuLV 3' LTR
7683Origin of replication
9302-8442 b-Lactmase coding sequence

Figure 20



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Figure 21(A). Gene Sequence of a Single Retrovector IgM Construct (SEQ ID NO:37)



- LTR = Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat Fusion
 Ψ EPR = Moloney Murine Leukemia Virus Psi Region and Extended Viral Packaging Region
 JC = J Chain Gene
 CMV = Simian Cytomegalovirus Promoter Region
 SP = Heavy Chain Signal Peptide
 HC = Mu Heavy Chain Gene
 IRES = Internal Ribosome Entry Site/α-Lactalbumin Signal Peptide
 LC = Kappa or Lambda Light Chain Gene
 RESE = RNA Export and Stability Element
 LTR = Moloney Murine Leukemia Virus Long Terminal Repeat

GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGTCATTAGTTCAT
 AGCCCATATATGGAGTCCCGCGTTACATAACTACGGTAAATGGCCCGCTGGCTGACC
 GCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAA
 TAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCACTTGGCA
 GTACATCAAGTGTATCATATGCCAAGTACGCCCCATTGACGTCAATGACGGTAAATG
 GCCCGCCTGGCATTATGCCAGTACATGACCTATGGGACTTTCTACTTGGCAGTACA
 TCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTGGCAGTACATCAATGGG
 CGTGGATAGCGGTTGACTCACGGGATTCCAAGTCTCCACCCATTGACGTCAATGG
 GAGTTGTTGGCACAAAATCAACGGACTTCAAATGTCGTAAACAACCTCCGCC
 CATTGACGCAAATGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTAA
 TAAAAGAGCCCACAACCCCTCACTCGCGCGCCAGTCTCCGATAGACTGCGTCGCC
 GGTACCCGTATCCCAAATAAGCCTCTTGCATCCGAATCGTGGCTCGCTGT
 TCCTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGTCTTCATTTGGG
 GGCTCGTCCGGGATTGGAGACCCCTGCCAGGGACCCACCGACCGGGAGGTA
 AGCTGGCCAGCAACTTATCTGTCTGCGATTGTCTAGTGTCTATGTTGATGTTAT
 GCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGAA
 CTGACGAGTTCTGAACACCCGGCGCAACCTGGGAGACGTCCCAGGGACTTGGGGC
 CGTTTTGTGGCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCGTCAGGATA
 TGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCTCCGTCTGAATTTC
 TTTCGGTTGGAACCGAAGCCGCGCTCTGTCTGCTGCAGCGCTGCAGCATGTTCTG
 TGTTGTCTCTGTCTGACTGTGTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTTAC
 CACTCCCTTAAGTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACACC
 AGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAAATGGCCAACC
 TTTAACGTCGGATGGCCCGAGACGGCACCTTAACCGAGACCTCATCACCCAGGTTAA
 GATCAAGGTCTTTCACCTGGCCCGATGGACACCCAGACCCAGGTCCCTACATCGTGA
 CCTGGGAAGCCTGGCTTTGACCCCCCTCCCTGGGTCAAGCCCTTGTACACCCTAAG
 CCTCCGCCTCCTCTCCATCCGCCCCGTCTCTCCCCCTGAACCTCCTCGTTGAC

FIGURE 21 (B)

CCCGCCTCGATCCTCCCTTATCCAGCCCTCACTCCTCTAGGCGCCGAATTCCGA
TCTGATCAAGAGACAGGATGAGAAGTCAAGATGAAGAACCATTGCTTTCTGGGGAGT
CCTGGCGGTTTATTAAGGCTGTCATGTGAAAGCCAAGAAGATGAAAGGATTGTC
TTGTTGACAACAAATGTAAGTGTGCCGGATTACTCCAGGATCATCGTCTTCGAA
GATCCTAATGAGGACATTGTGGAGAGAAACATCCGAATTATTGTTCTCTGAACAAACAG
GGAGAATATCTGTGATCCCACCTCACCATGAGAACAGAGATTGTGTACCATTGTCTG
ACCTCTGTAAAAAATGTGATCCTACAGAAGTGGAGCTGGATAATCAGATAGTTACTGCT
ACCCAGAGCAATATCTGTGATGAAGACAGTGCTACAGAGACCTGCTACACTTATGACAG
AAACAAGTGTACACAGCTGTGGCCACTCGTATATGGTGGTAGACCAAATGGTGG
AAACAGCCTAACCCCCAGATGCCTGCTATCCTGACTAAAGATCCCTATGGCTATTGGCCA
GGTTCAATACTATGTATTGCCCTATGCCATATAGTATTCCATATATGGGTTTCCTAT
TGACGTAGATAGCCCCTCCAATGGCGGTCCCATATACCATATATGGGCTTCCTAAT
ACCGCCCATAGCCACTCCCCATTGACGTCAATGGTCTCTATATGGTCTTCCTATT
GACGTCAATGGCGGTCTATTGACGTATATGGCGCTCCCCATTGACGTCAATTAC
GGTAAATGGCCCGCTGGCTCAATGCCATTGACGTCAATAGGACCACCCACCATGAC
GTCAATGGGATGGCTATTGCCATTGACGTCAATAGGACCACCCACCATGAC
TGACGGTAAATGGCCCATTGGCAGTACATCAATATCTATTAAATAGTAACGGCAAGT
ACATTACTATTGGAAGTACGCCAGGGTACATTGGCAGTACTCCCATTGACGTCAATGGC
GGTAAATGGCCCGCATGGCTGCCAAGTACATCCCCATTGACGTCAATGGGAGGGCA
ATGACGCCAAATGGCGTCCATTGACGTAAATGGCGGTAGGCGTGCTAATGGGAGGT
CTATATAAGCAATGCTGTTAGGGAACCGCCATTCTGCCTGGGACGTGGAGGAGCT
CGAAAGCTTAGGACCTCACATGGGATGGAGCTGTATCATCCTCTTGGTAGCAACA
GCTACAGGTGTCACTCCGAGGTCCAATGGTGGAGAGCGGTGGAGGTGTTGCAACC
TGGCCGGTCCCTGCGCTGTCCTGCTCCGCATCTGGCTTCGATTTCACCATATTGGA
TGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGGATTGGAGAAATTCA
GATAGCAGTACGATTAACATGCGCGTCTCTAAAGGATAGATTACAATATCGCGAGA
CAACGCCAAGAACACATTGTTCTGCAAATGGACAGCCTGAGACCCGAAGACACCGGG
TCTATTTTGCAAGCCTTACTTCGGCTCCCTGGTTGCTTATTGGGCCAAGGG
ACCCCGGTACCGTCTCCTCAGGGAGTGCATCGCCCCAACCTTCCCTCGTCTC
CTGTGAGAATTCCCCGTGGATACGAGCAGCGTGGCGTTGGCTGCCTCGCACAGGACT
TCCTTCCGACTCCATCACTTGTCTGGAAATACAAGAACAACTCTGACATCAGCAGT
ACCCGGGGCTCCATCAGTCTGAGAGGGGAAGTACGAGCCACCTCACAGGTGCT
GCTGCCCTCCAAGGACGTATGCAGGGCACAGACGAACACGTGGTGTGCAAAGTCCAGC
ACCCCAACGGCAACAAAGAAAAGAACGTGCCCTTCCAGTGATTGCCAGCTGCCCTCC
AAAGTGAGCGTCTCGTCCACCCCGCAGGGCTTCTCGCAACCCCGCAAGTCCAA
GCTCATCTGCCAGGCCACGGTTTCAGTCCCCGGCAGATTAGGTGTCCTGGCTGCGCG
AGGGGAAGCAGGTGGGTCTGGCGTACCCACGGACCAGGTGCAGGCTGAGGCCAAGAG
TCTGGGCCACGACCTACAAGGTGACCAGCACACTGACCATCAAAGAGAGCGACTGGCT
CGGCCAGAGCATGTTCACCTGCCGTGGATCACAGGGCCTGACCTCCAGCAGAATG
CGTCCTCCATGTGTCCCCGATCAAGACACAGCCATCCGGTCTCGCCATCCCCCA
TCCTTGCCAGCATCTCCTCACCAAGTCCACCAAGTTGACCTGCCCTGGTCACAGACCT
GACCACCTATGACAGCGTGACCATCTCCTGGACCCGCCAGAATGGCGAAGCTGTGAAA
CCCACACCAACATCTCCGAGAGCCACCCCAATGCCACTTCAGCGCCGTGGGTGAGGCC
AGCATCTGCGAGGATGACTGGAATTCCGGGAGAGGTTACGTGCACCGTGACCCACAC

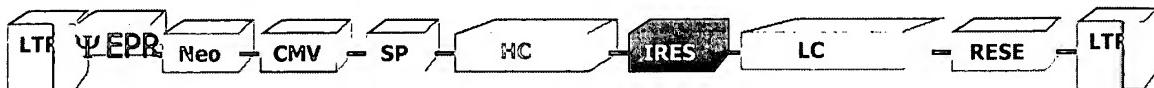
FIGURE 21 (C)

AGACCTGCCCTGCCACTGAAGCAGACCATCTCCGGCCAAGGGGTGGCCCTGCACA
GGCCCGATGTCTACTTGCTGCCACCAGCCGGAGCAGCTGAACCTGCAGGAGTCGGCC
ACCATCACGTGCCCTGGTACGGGCTCTCTCCCGCGACGCTTCGTGCAGTGGATGCA
GAGGGGGCAGCCCTGTCCCCGGAGAAGTATGTGACCAGCGCCCAATGCCTGAGCCCC
AGGCCCCAGGCCGGTACCTGCCACAGCATCCTGACCGTGTCCGAAGAGGAATGGAAC
ACGGGGGAGACCTACACCTGCGTGGCCATGAGGCCCTGCCAACAGGGTCACCGAGAG
GACCGTGGACAAGTCCACCGGTAAACCCACCCGTACAACGTGTCCCTGGTATGTCCG
ACACAGCTGGCACCTGCTACTGAGATCTCTGCAGAAACGGCCTAGGTTGGAAATT
GCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCGAAGCCGCTTGAATAAGGCCGGT
GTGCGTTGTCTATATGTTATTTCCACCATATTGCCGTCTTGGCAATGTGAGGGCC
CGGAAACCTGGCCCTGTCTTGCAGGACATTCTAGGGTCTTCCCCTCGCCAA
AGGAATGCAAGGTCTGTGAATGCGAAGGAAGCAGTCCCTCTGGAAGCTCTTGAA
GACAAACAACGTCTGTAGCGACCTTGAGCGAGCACCTGCAAAGGCCGACAACCCCA
TGCCTCTGCCAAAAGCCACGTGTATAAGATAACACCTGCAAAGGCCGACAACCCCA
GTGCCACGTTGTGAGTTGGATAGTTGTGAAAGAGTCAAATGGCTCTCAAGCGTAT
TCAACAAGGGCTGAAGGATGCCAGAAGGTACCCATTGTATGGATCTGATCTGGGG
CCTCGGTGCACATGTTACATGTGTTAGTCGAGGTTAAAAAAACGTCTAGGCC
GAACCAACGGGACGTGGTTTCTTGAACACAGATGATAATATGGCTCTTGTC
TCTCTGCTCTGGTAGGCATCTTCCATGCCACCCAGGCCGACATCCAGCTGACCCA
GAGCCAAGCAGCCTGAGGCCAGCGTGGTGACAGAGTGACCATCACCTGTAAGGCC
GTCAGGATGTGGTACTCTGTAGCCTGGTACCGAGCAGAACCCAGGTAAAGGCTCAAAG
CTGCTGATCTACTGGACATCCACCCGGCACACTGGTGTGCAAGCAGATTAGCGGTAG
CGGTAGCGGTACCGACTCACCTCACCACAGCAGCCTCCAGCCAGAGGACATGCC
CCTACTACTGCCAGCAATATAGCCTCTATCGGTGTTGCCAAGGGACCAAGGTGGAA
ATCAAACGAACTGTGGCTGCACCATCTGTCTTCACTTCCGCCATCTGATGAGCAGTT
GAAATCTGGAACTGCCTCTGTTGTGCTGAATAACTCTATCCAGAGAGGCCA
AAAGTACAGTGGAAAGGTGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGT
GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCGTGACGCTGAGCAAAGC
AGACTACGAGAAACACAAAGTCTACGCCCTGCAAGTCACCCATCAGGGCTGAGCTCGC
CCGTACAAAGAGCTTCAACAGGGAGAGTGTAGATCTGTTAACCTCTAGGCTCGAGTT
CGACATCGATAATCAACCTCTGGATTACAAAATTGTGAAAGATTGACTGGTATTCTTA
ACTATGTTGCTCTTACGCTATGTGGATACGCTGCTTAATGCCCTTGATCATGCT
ATTGCTTCCCGTATGGCTTCACTTCTCCTTGTATAAATCCTGGTTGCTGTCTCT
TTATGAGGAGTTGTGGCCGTTGTCAGGCAACGTGGCGTGGTGTGCAGTGTGTTGCTG
ACGCAACCCCCACTGGTGGGCATTGCCACCCACCTGTCAAGCTCCTTCCGGACTTTC
GCTTCCCCCTCCCTATTGCCACGGCGGAACTCATGCCGCCTGCCCTGCCGCTGCTG
GACAGGGCTGGCTGTTGGCACTGACAATTCCGTGGTGTGCGGGAAATCATCGT
CCTTCCCTGGCTGCTGCCCTGTGTTGCCACCTGGATTCTGCGCGGAGCTCCTCTGC
TACGTCCCTCGGCCCTCAATCCAGGGACCTCCTCCCGCGGCTGCTGCCGCTCT
GCCGCCTCTCCCGCTTCCGCCTGCCCTCAGACGAGTCGGATCTCCCTTGGCCG
CCTCCCCGATCGATAAAATAAAAGATTATTTAGTCTCCAGAAAAAGGGGGAAATGA
AAGACCCCACCTGTAGGTTGGCAAGCTAGCTTAAGTAACGCCATTGCAAGGCATGG
AAAAATACATAACTGAGAATAGAGAAGTTAGATCAAGGTCAAGGAACAGATGGAACAGC
TGAATATGGCCAAACAGGATATCTGTGGTAAGCAGTCAGGCCCTGGCTCAGGGCCAA

FIGURE 21 (D)

GAACAGATGGAACAGCTGAATATGGGCCAACAGGATATCTGTGGTAAGCAGTTCCCTGC
CCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTCT
AGAGAACCATCAGATGTTCCAGGGTGCCCAAGGACCTGAAATGACCCTGTGCCTTAT
TTGAACTAACCAATCAGTCGCTTCTCGCTTCTGTCGCGCGCTTCTGCTCCCCGAGCT
CAATAAAAGAGCCCACAACCCCTCACTCGGGCGCCAGTCCTCCGATTGACTGAGTCGC
CCGGGTACCCGTATCCAATAAACCTCTTGAGTTGCATCCGACTTGTGGTCTCGCT
GTTCCCTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTAGCGGGGTCTTCATT

Figure 22(A). Gene Sequence of a Double Retrovector IgM Heavy and Light Chain Construct (SEQ ID NO:38).



LTR =	Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat Fusion
Ψ EPR =	Moloney Murine Leukemia Virus Psi Region and Extended Viral Packaging Region
Neo =	Neomycin Resistance Gene
CMV =	Simian Cytomegalovirus Promoter Region
SP =	Heavy Chain Signal Peptide
HC =	Mu Heavy Chain Gene
IRES =	Internal Ribosome Entry Site/α-Lactalbumin Signal Peptide
LC =	Kappa or Lambda Light Chain Gene
RESE =	RNA Export and Stability Element
LTR =	Moloney Murine Leukemia Virus Long Terminal Repeat

GTTGACATTGATTATTGACTAGTTATTAAATAGTAATCAATTACGGGGTCAATTAGTTCAT
 AGCCCATAATGGAGTTCCCGCTTACATAACTTACGGTAAATGGCCCGCTGGCTGACC
 GCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAA
 TAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTACGGTAAACTGCCACTTGGCA
 GTACATCAAGTGTATCATATGCCAAGTACGCCCTATTGACGTCAATGACGTAAATG
 GCCCGCCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCTACTTGGCAGTACA
 TCTACGTATTAGTCATCGCTATTACCATGGTATGCGGTTTGGCAGTACATCAATGGG
 CGTGGATAGCGGTTTGAUTCACGGGATTCCAAGTCTCCACCCATTGACGTCAATGG
 GAGTTGTTTGGCACCAAAATCAACGGACTTCAAATGTCGAACAACCTCGGCC
 CATTGACGCAAATGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTCAA
 TAAAAGAGCCCACAACCCCTACTCGCGCGCAGTCTCCGATAGACTGCGTCGCCCG
 GGTACCCGTATCCCAATAAAGCCTTGTGTTGCATCCGAATCGTGGCTCGCTGT
 TCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGTCTTCATTTGGG
 GGCTCGTCCGGATTGGAGACCCCTGCCAGGGACCACCGACCCACCACGGGAGGTA
 AGCTGGCCAGCAACTATCTGTCTGTCCGATTGTCTAGTGTCTATGTTGATGTTAT
 GCGCCTGCGTCTGTACTAGTTAGCTAAGTCTGTATCTGGCGGACCCGTGGTGGAA
 CTGACGAGTTCTGAACACCCGGCGCAACCTGGGAGACGTCCCAGGGACTTGGGGC
 CGTTTTGTGGCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCGTCAAGGATA
 TGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCTCCGTCTGAATTGG
 TTTCGGTTGGAACCGAAGCCGCGCTTGTCTGCTGCAGCGCTGCAGCATCGTTCTG
 TGTTGTCTGTGACTGTGTTCTGTATTGTCTGAAAATTAGGCCAGACTGTTAC
 CACTCCCTTAAGTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTACAACC
 AGTCGGTAGATGTCAAGAACGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGCCAAC
 TTTAACGTCGGATGCCCGAGACGGCACCTTAACCGAGACCTCATCACCCAGGTTAA

FIGURE 22 (B)

GATCAAGGTTTCACCTGGCCCGATGGACACCCAGACCAGGTCCCCTACATCGTGA
CCTGGGAAGCCTGGCTTTGACCCCCCTCCCTGGGTCAAGCCCTTGACACCCTAAG
CCTCCGCCTCCTCTCCATCCGCCCCGTCTCTCCCCCTGAACCTCCTCGTTGAC
CCCGCCTCGATCCTCCCTTATCCAGCCCTCACTCCTCTAGGCGCCGAAATTCCGA
TCTGATCAAGAGACAGGATGAGGATCGTTCGATGATTGAACAAGATGGATTGCACGC
AGGTTCTCCGGCGCTGGGTGGAGAGGCTATTGGCTATGACTGGCACAACAGACAA
TCGGCTGCTCTGATGCCCGTGTCCGGCTGTCAGCGCAGGGCGCCGGTTCTTTT
GTCAAGACCGACCTGTCCGGTGCCTGAATGAAC TGCAAGGACGAGGAGCGCG
GAAGGGACTGGCTGCTATTGGCGAAGTGCCGGGCAGGATCTCCTGTATCTCACCT
GCTCCTGCCAGAAAAGTATCCATCATGGCTGATGCAATGCCGGCTGCATACGCTTGA
TCCGGCTACCTGCCCATCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTC
GGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGCG
CCAGCCGAACTGTTGCCAGGCTCAAGGCCGCATGCCGACGGCGAGGATCTGTCGT
GACCCATGGCGATGCCCTGCTGCCAATATCATGGTGGAAAATGCCGCTTCTGGAT
TCATCGACTGTGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACC
CGTGTATTGCTGAAGAGCTGGCGCGAATGGGCTGACCGCTCTCGTGTCTTACGG
TATGCCGCTCCGATTGCAAGCGCATGCCCTCATGCCCTTGTGACGAGTTCTTCT
GAGGATCCCTATGGCTATTGCCAGGTTCAATACTATGTATTGCCCTATGCCATATAG
TATTCCATATATGGGTTTCCTATTGACGTAGATAGCCCCTCCAATGGCGGTCCCAT
ATACCATATATGGGCTTCCTAATACGCCATAGCCACTCCCCATTGACGTCAATGG
TCTCTATATATGGTCTTCCTATTGACGTATATGGCGGTCTATTGACGTATATGGC
GCCTCCCCATTGACGTCAATTACGGTAATGCCCTGGCTCAATGCCATTGACG
TCAATAGGACCACCCACCATTGACGTCAATGGGATGGCTATTGCCATTCAATCCGT
TCTCACGCCCTATTGACGTCAATGACGGTAATGCCCTGGCAGTACATCAATA
TCTATTAATAGTAACCTGGCAAGTACATTACTATTGGAAGTACGCCAGGGTACATTGGC
AGTACTCCCATTGACGTCAATGGCGGTAAATGCCCGCGATGGCTGCCAAGTACATCCC
CATTGACGTCAATGGGAGGGCAATGACGCAAATGGCGTTCCATTGACGTAAATGGG
CGTAGGCGTGCCTAATGGAGGTCTATATAAGCAATGCTCGTTAGGAACCGCCATT
CTGCCTGGGACGTCGGAGGAGCTCGAAAGCTTAGGACCTACCATTGGGATGGAGCTGT
ATCATCCTCTTGTAGCAACAGCTACAGGTGTCCTCCGAGGTCCAATGGTGG
GAGCGGTGGAGGTGTTGCAACCTGCCCGTCCCTGCGCCTGCTGCCATCTG
GCTTCGATTCACCACATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTT
GAGTGGATTGGAGAAATTCCAGATAGCAGTACGATTAACATGCGCGTCTCTAAA
GGATAGATTACAATATCGCGAGACAACGCCAAGAACACATTGTTCTGCAAATGGACA
GCCTGAGACCCGAAGACACCGGGTCTATTGTGCAAGCCTTACTCGGCTTCCCC
TGGTTGCTTATTGGGCAAGGGACCCGGTACCGTCTCTCAGGGAGTGACATCCGC
CCCAACCCCTTCCCCCTCGTCTCTGTGAGAATTCCCCGTGGATACGAGCAGCGTGG
CCGTTGGCTGCCCTCGCACAGGACTCCCTCCGACTCCATCACTTGTCTGAAATAC
AAGAACAACTCTGACATCAGCAGTACCCGGCTTCCCATCAGTCCTGAGAGGGGCAA
GTACGCAGCCACCTCACAGGTGCTGCTGCCCTCAAGGACGTATGCAGGGCACAGACG
AACACGTGGTGTGCAAAGTCCAGCACCCAAACGGCAACAAAGAAAAGAACGTGCTT
CCAGTGATTGCCAGCTGCCCTCCAAAGTGAGCGTCTCGTCCCACCCCGCACGGCTT
CTCGCAACCCCGCAAGTCAAGTCTGCAAGGCCACGGTTCAAGTCCCCGG

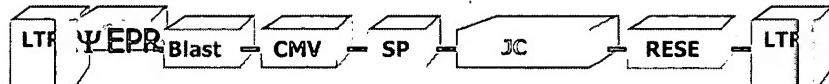
FIGURE 22 (C)

AGATTCAAGGTGCTGGCTGCGCGAGGGGAAGCAGGTGGGTCTGGCGTCACACGGAC
CAGGTGCAGGCTGAGGCCAAAGAGTCTGGGCCACGACCTACAAGGTGACCAGCACACT
GACCATCAAAGAGAGCGACTGGCTGGCCAGAGCATGTTCACCTGCCCGTGGATCACA
GGGGCCTGACCTTCCAGCAGAATGCGTCCTCCATGTGTCCCCGATCAAGACACAGCC
ATCCGGGTCTCGCCATCCCCCATCCTTGCAGCATCTCCTCACCAAGTCCACCAA
GTTGACCTGCCTGGTCACAGACCTGACCGACCTATGACAGCGTGACCATCTCCTGGACCC
GCCAGAAATGGCGAAGCTGTGAAAACCCACACCAACATCTCCGAGAGGCCACCCCAATGCC
ACTTTCAGCGCCGTGGGTGAGGCCAGCATCTGCAGGATGACTGGAATTCCGGGAGAG
GTTCACGTGACCGTGACCCACACAGACCTGCCACTGAAGCAGACCATCTCCC
GGCCAAGGGGTGGCCCTGCACAGGCCGATGTCTACTTGCTGCCACCAGCCCAGGGAG
CAGCTAACCTGCGGGAGTCGGCCACCATCACGTGCCTGGTACGGCTTCTCTCCC
GGACGTCTCGTCAGTGGATGCAGAGGGCAGCCCTGTCCCCGGAGAAGTATGTGA
CCAGGCCCAATGCCTGAGCCCCAGGCCGGTACTCGCCACAGCATTG
ACCGTGTCCGAAGAGGAATGGAACACGGGGGAGACCTACACCTGCAGGCCATGAGGC
CCTGCCAACAGGGTACCGAGAGGACCGTGGACAAGTCCACCGTAAACCCACCTGT
ACAACGTGTCCCTGGTCATGTCGACACAGCTGGCACCTGCTACTGAGATCTGAGA
AACCGGTCTAGGTTGGAATTGCCCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCC
GAAGCCGCTTGAATAAGGCCGGTGTGCGTTGTCTATATGTTATTTCACCATATTG
CCGTCTTGGCAATGTGAGGGCCCGAACCTGGCCCTGTCTTGTACGAGCATTCC
TAGGGTCTTCCCTCTGCCAACAGGAATGCAAGGTCTGTGAATGTCGTGAAGGAAG
CAGTTCTCTGAAAGCTCTGAAGACAAACACGTCTGTAGCGACCCTTGCAGGCAG
CGGAACCCCCACCTGGCGACAGGTGCCTCTGCCAAAAGCCACGTGTATAAGATAC
ACCTGCAAAGGCCACAACCCAGTGCACAGTGGTGAAGGATAGTTGTGAAAGAG
TCAAATGGCTCCTCAAGCGTATTCAACAAGGGCTGAAGGATGCCAGAAGGTACCC
CATTGTATGGATCTGATCTGGGCCTCGGTGCACATGCTTACATGTGTTAGTCGAG
GTTAAAAAAACGTCTAGGCCCGAACACGGGACGTGGTTCTTGAAACAC
GATGATAATATGGCTCCTTGTCTCTGCTCTGGTAGGCATCCTATTCCATGCCAC
CCAGGCCGACATCCAGCTGACCCAGGCCAAGCAGCCTGAGGCCAGCGTGGTGACA
GAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGTACTCTGTAGCCTGGTACCA
CAGAACGCCAGGTAAAGGCTCAAAGCTGTGATCTACTGGACATCCACCCGGCACACTGG
TGTGCCAAGCAGATTAGCGGTAGCGGTAGCGGTACCGACTTCACCTCACCACAGCA
GCCTCCAGCCAGGGACATGCCACCTACTACTGCCAGCAATATAGCCTATCGGT
TTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGCTT
CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCCTGTGTGCGCTGCTGA
ATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCAATCG
GGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG
CAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCC
TCACCCCATCAGGGCCTGAGCTGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
ATCTGTTAACCTAGGCTCGAGTCACAGAGCAGGACAGCACCTACAGCCTCAG
CAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCC
TCACCCCATCAGGGCCTGAGCTGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
ATCTGTTAACCTAGGCTCGAGTCACAGAGCAGGACAGCACCTACAGCCTCAG
GTGAAAGATTGACTGGTATTCTTAACATGTTGCTCCTTACGCTATGTGGATAACGCT
GCTTTAATGCCCTTGTATCATGCTATTGCTTCCCGTATGGCTTCACTTCTCCT
GTATAAACTCTGGTTGCTGTCTTTATGAGGAGTTGTGGCCCGTGTCAAGGAAACGTG
GCGTGGTGTGCACTGTGTTGCTGACGCAACCCCCACTGGTGGGGCATTGCCAC
TGTCAAGCTCCTTCCGGACTTGCCTTCCCCCTCCATTGCCACGGCGGAACCTAC

FIGURE 22 (D)

CGCCGCCTGCCTGCCGCTGGACAGGGCTGGCTGTTGGGCACTGACAATTCCG
TGGTGTTCGGGGAAATCATCGCCTTCCTGGCTGCTGCCTGTGTTGCCACCTGG
ATTCTCGCGGGACGTCTGCTACGTCCTCGGCCCTCAATCCAGCGGACCTCC
TTCCCGCGCCTGCTGCCGGCTCGGCCCTTCGGCTCTCGCCTCGCCCTCAGA
CGAGTCGGATCTCCCTTGGGCCCTCCCCGATCGATAAAATAAAAGATTTATTTA
GTCTCCAGAAAAAGGGGGAATGAAAGACCCCACCTGAGGTTGGCAAGCTAGCTAA
GTAACGCCATTTGCAAGGCATGAAAAAATACATAACTGAGAATAGAGAAGTCAGATC
AAGGTCAAGAACAGATGGAACAGCTGAATATGGGCCAACAGGATATCTGTGTAAGCA
GTTCCCTGCCCGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAACAGG
ATATCTGTGTAAGCAGTTCCTGCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGAT
GCGGTCCAGCCCTCAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGCCCCAAGG
ACCTGAAATGACCCCTGTGCCTTATTGAACTAACCAATCAGTCGCTCTCGCTCTGT
TCGCGCGCTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGC
CAGTCCTCCGATTGACTGAGTCGCCGGTACCCGTATCCAATAAACCCCTTGCAG
TTGCATCCGACTTGTGGTCTCGCTGTTCCCTGGGAGGGTCTCCTCTGAGTGATTGACTA
CCCGTCAGCGGGGGCTTCATT

Figure 23(A) Gene Sequence of a Double Retrovector IgM J Chain Construct (SEQ ID NO:39).



- LTR = Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat Fusion
 Psi EPR = Moloney Murine Leukemia Virus Psi Region and Extended Viral Packaging Region
 Blast = Blasticidin Resistance Gene
 CMV = Simian Cytomegalovirus Promoter Region
 SP = J Chain Signal Peptide
 JC = J Chain Gene
 RESE = RNA Export and Stability Element
 LTR = Moloney Murine Leukemia Virus Long Terminal Repeat

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GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGCATTAGTTCAT
AGCCCATATATGGAGTTC CGCGT TACATAACTTACGGTAAATGGCCCGCTGGCTGACC
GCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCAGTAGTAACGCCAA
TAGGGACTTCCATTGACGTCAATGGGTGGAGTATTACGGTAAACTGCCACTTGGCA
GTACATCAA GTGTATCATATGCCAAGTACGCCCTATTGACGTCAATGACGGTAAATG
GCCCGCCTGGCATTATGCCAGTACATGACCTTATGGACTTCCACTTGGCAGTACA
TCTACGTATTAGTCATCGCTATTACCATGGTATGCGGTTTGGCAGTACATCAATGGG
CGTGGATAGCGGTTGACTCACGGGATTCCAAGTCTCCACCCATTGACGTCAATGG
GAGTTTGTGGCACCAAAATCAACGGACTTCCAAAATGTCGTAACAACCTCCGCC
CATTGACGCAAATGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTCAA
TAAAAGAGCCCACAACCCCTCACTCGCGGCCAGTCTCCGATAGACTGCGTCGCCCG
GGTACCCGTATTCCAATAAGCCTCTTGCTGTTGCATCCGAATCGGGTCTCGCTGT
TCCTGGGAGGGTCTCTGAGTGATTGACTACCCACGACGGGGTCTTCATTGGG
GGCTCGTCCGGGATTGGAGACCCCTGCCAGGGACCACGACCCACCACGGGAGGTA
AGCTGGCCAGCAACTTATCTGTCTGTCGATTGTCTAGTGTCTATGTTGATGTTAT
GCGCCTCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGACCGTGGAA
CTGACGAGTTCTGAACACCCGGCGCAACCCCTGGGAGACGTCCCAGGGACTTGGGGC
CGTTTTGTGGCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATA
TGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCGTCTGAATTGGC
TTTCGGTTGGAACCGAAGCCCGCGTCTGTCTGCTGCAGCGCTGCAGCATCGTCTG
TGTTGTCTGTCTGACTGTGTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTTAC
CACTCCCTTAAGTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTACAACC
AGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGCCAACC
TTAACGTCGGATGGCCCGAGACGGCACCTTAACCGAGACCTCATCACCCAGGTTAA
GATCAAGGTCTTTCACCTGGCCCGATGGACACCCAGACCCAGGTCCCTACATCGTGA
CCTGGGAAGCCTGGCTTTGACCCCCCTCCCTGGGTCAAGCCCTTGTACACCCTAAG
CCTCCGCCTCCTCCATCCGCCCCGTCTCCCCCTTGAACCTCCTCGTTCGAC

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FIGURE 23 (B)

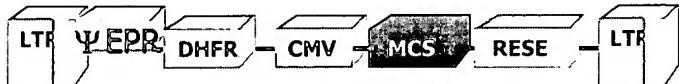
CCCGCCTCGATCCTCCCTTATCCAGCCCTCACTCCTCTAGGCGCCGAATTCATG
GCCAAGCCTTGTCTCAAGAAGAACATCCACCCATTGAAAGAGCAACGGCTACAATCAA
CAGCATCCCCATCTCTGAAGACTACAGCGTCGCCAGCGCAGCTCTCTAGCGACGGCC
GCATCTTCACTGGTGTCAATGTATATCATTTACTGGGGGACCTTGTGCAGAACTCGTG
GTGCTGGGCACTGCTGCTGCTGCCAGCTGGCAACCTGACTGTATCGTCGGATCGG
AAATGAGAACAGGGCATCTTGAGCCCCTGCCAGGGACAGGTGCTCTCGATC
TGCATCCTGGGATCAAAGCCATACTGAAGGACAGTGTGATGGACAGCCACGGCAGTTGGG
ATTCGTGAATTGCTGCCCTGGTTATGTGTGGGAGGGCTAAGCACTGGATCCCTATG
GCTATTGCCAGGTTCAATACTATGTATTGCCCTATGCCATATAGTATTCCATATATG
GGTTTCCTATTGACGTAGATAGCCCCTCCAATGGCGGTCCCATAACCATATATGG
GGCTCCTAATACGCCATAGCCACTCCCCATTGACGTCAATGGCTCTATATATGG
TCTTCCTATTGACGTATATGGCGGTCTATTGACGTATATGGCCCTCCCCATTG
ACGTCAATTACGGTAAATGGCCCGCTGGCTCAATGCCATTGACGTCAATAGGACCAC
CCACCAATTGACGTCAATGGGATGGCTATTGCCATTCCGTTCTCACGCCCT
ATTGACGTCAATGACGGTAAATGGCCCACTTGGCAGTACATCAATATCTATTAAAGTA
ACTTGGCAAGTACATTACTATTGGAAGTACGCCAGGGTACATTGGCAGTACTCCATTG
ACGTCAATGGCGGTAAATGGCCCGCGATGGCTGCCAAGTACATCCCCATTGACGTCAAT
GGGGAGGGGCAATGACGAAATGGCGTTCCATTGACGTAATGGCGGTAGGCGTGCC
TAATGGGAGGTCTATATAAGCAATGCTCGTTAGGAAACGCCATTCTGCCTGGGAGC
TCGGAGGAGCTCGAAAGCTTGAAGTCAAGATGAAGAACCATTTGCTTCTGGGAGTC
CTGGCGGTTTATTAAAGGCTGTCATGTGAAAGCCAAGAACAGATGAAAGGATTGTTCT
TGTTGACAACAAATGTAAGTGTGCCCGGATTACTTCCAGGATCATCCGTTCTCGAAG
ATCCTAATGAGGACATTGAGGAAACATCCGAATTATTGCTCTGAACAAACAGG
GAGAACATCTGATCCCACCTCACCATTGAGAACCAAGGATTGCTGACATTGCTGA
CCTCTGAAAAAAATGTGATCCTACAGAAGTGGAGCTGGATAATCAGATAGTTACTGCTA
CCCAGAGCAATATCTGTGATGAAGACAGTGCTACAGAGACCTGCTACACTTATGACAGA
AACAAAGTGTACACAGCTGCTGCCACTCGTATATGGGGTGGAGACCAAAATGGTGG
AACAGCCTAACCCCAAGATGCCCTGCTACCTGACTAAGATCTGTTAACGGCCTAGGT
TTAAACTCGAGTTGACATCGATAATCAACCTCTGGATTACAAAATTGAAAGATTG
ACTGGTATTCTTAACTATGTTGCTCCTTACGCTATGTGGATACGCTGCTTAATGCC
TTTGTATCATGCTATTGCTCCCGTATGGCTTACCTTCTCCTGTATAAAATCCT
GGTTGCTGTCTTTATGAGGAGTTGTGGCCCGTGTGAGGCAACGTGGCGTGGTGC
ACTGTGTTGCTGACGCAACCCCCACTGGTTGGGCATTGCCACCACTGTGAGCTCCT
TTCCGGGACTTCGCTTCCCCCTCCATTGCCACGGCGAACATGCCGCTGCC
TTGCCCGCTGGACAGGGCTGGCTGGCTGGACTGACAATTCCGTGGTGTGCG
GGGAAATCATCGTCCTTCCATTGGCTGCTGCCCTGTGTTGCCACCTGGATTCTGCGCG
GACGTCTCTGCTACGCTCCATTGCCCTCAATCCAGCGGACCTCCTCCCGCG
TGCTGCCGGCTTGCGGCCCTTCCGCGTCTCGCCTCGCCCTCAGACGAGTCGGATC
TCCCTTGGGCCCTCCCGCATCGATAAAATGGGAAAGATTGTTACTGCTCCAGAAA
AAGGGGGGAATGAAAGACCCCCACTGTAGGTTGGCAAGCTAGCTTAAGTAACGCCATT
TTGCAAGGCATGGAAAAATACATACTGAGAACAGGAGATCTGTGGTAAGCAGTTCTGCC
CAGATGGAACAGCTGAATATGGCCAAACAGGAGATCTGTGGTAAGCAGTTCTGCC
GGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGCCAAACAGGAGATCTGTGGT

FIGURE 23 (C)

AAGCAGTTCTGCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCC
CTCAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGCCCAAGGACCTGAAATGA
CCCTGTGCCTTATTGAACTAACCAATCAGTCGCTTCTCGCTTCTGTTCGCGCTTC
TGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCCAGTCCTCCGA
TTGACTGAGTCGCCCCGGGTACCCGTATCCAATAAACCCCTTGCAGTTGCATCCGAC
TTGTGGTCTCGCTGTTCTGGAGGGTCTCCTCTGAGTGATTGACTACCCGTAGCGG
GGGTCTTCATT

FIGURE 24 (A)

Mouse dihydrofolate reductase retrovector gene construct (SEQ ID NO:40).



- LTR = Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat Fusion
Ψ EPR = Moloney Murine Leukemia Virus Psi Region and Extended Viral Packaging Region
DHFR = Mouse Dihydrofolate Reductase Gene
CMV = Simian Cytomegalovirus Promoter Region
MCS= Multiple Cloning Site (Gene Insertion Site)
RESE = RNA Export and Stability Element
LTR = Moloney Murine Leukemia Virus Long Terminal Repeat

1 GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCAATTAGTTCAAGCCCATAATGGAGTTCCCGCGTTACATAACTTACGGTAAATGGCCCGCTGGCTGA
CCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAAGTAACGCC
AATAGGGACTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCACTTGG
CAGTACATCAAGTGTATCATATGCCAAGTACGCCCTATTGACGTCAATGACGGTAAA
TGGCCCGCTGGCATTATGCCAGTACATGACCTTATGGGACTTCCACTTGGCAGTA
CATCTACGTATTAGTCATCGCTATTACCATGGTATGGCTGGGAGGTACATCAATG
GGCGTGGATAGCGGTTGACTCACGGGATTCCAAGTCTCCACCCATTGACGTCAAT
GGGAGTTGTTGGCACCAAAATCAACGGGACTTCCAAATGTCGAACAACCTCCGC
CCCATTGACGCAAATGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTC
AATAAAAGAGCCCACAACCCCTCACTCGCGCGCCAGTCTCCGATAGACTCGTCGCC
CGGGTACCGTATTCCAATAAGCCTTGTGCTGGCATCCGAATCGTGGCTCGCT
GTTCTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGTCTTCATTG
GGGGCTCGTCCGGATTGGAGACCCCTGCCAGGGACCACCGACCCACCACGGGAGG
TAAGCTGGCCAGCAACTATCTGTCTGCGATTGCTAGTGTCTATGTTGATGTT
ATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGGGACCCGTGGTGG
AACTGACGAGTTCTGAACACCCGGCGCAACCCCTGGGAGACGTCCAGGGACTTGGGG
GCCGTTTGTGGCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCGTAGGA
TATGTGGTTCTGGTAGGAGACGAGAACCTAAACAGTCCCGCTCCGTCTGAATT
GCTTCGGTTGGAACCGAAGCCCGCGTCTGTGCTGCTGCAGCGCTGCAGCATCGTC
TGTGTTGCTCTGTGACTGTGTTCTGTATTGCTGAAATTAGGGCCAGACTGTT
ACCACTCCCTTAAGTTGACCTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAA
CCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTGTGCTGCTGCAGCATCGTC
CCTTAACTGTCGGATGGCCGCGAGACGGCACCTTAACCGAGACCTCATCACCCAGGTT
AAGATCAAGGTCTTTCACCTGGCCGATGGACACCCAGACCAGGTCCCCTACATCGT
GACCTGGGAAGCCTTGGCTTTGACCCCCCTCCGTCAAGCCCTTGTACACCCCTA

FIGURE 24 (B)

AGCCTCCGCCTCCTCTTCCATCCGCCCGTCTCTCCCCCTTGAAACCTCCTCGTTCG
ACCCCGCCTCGATCCTCCCTTATCCAGCCCTCACTCCTCTAGGCGCCGGAATTCC
GATCTGATCAAGAGACAGGGATGACCTAGGCTTGTCAAAGCTTATCCCCGCTGCCA
TCATGGTTGACCATTGAACTGCATCGTCCGCTGTCAGGAAAGATATGGGGATTGGCAAG
AACGGAGACCTACCCCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCAAAGAATGAC
CACAAACCTCTCAGTGGAAAGTAAACAGAATCTGGTATTGGTAGGAAAACCTGGT
TCTCCATTCTGAGAAGAATCGACCTTAAAGGACAGAATTAATATAGTTCTCAGTAGA
GAACCTCAAAGAACCAACGAGGAGCTCATTGCAAAAGTTGGATGATGCCCT
AAGACTTATTGAACAAACCGGAATTGGCAAGTAAAGTAGACATGGTTGGATAGTCGGAG
GCAGTTCTGTTACCAGGAAGCCATGAATCAACCAGGCCACCTCAGACTCTTGTGACA
AGGATCATGCAGGAATTGAAAGTGACACGTTTCCCAGAAATTGATTTGGGAAATA
TAAACTCTCCAGAATACCCAGCGTCCTCTGAGGTCCAGGAGGAAAAGGCATCA
AGTATAAGTTGAAGTCTACGAGAAGAAAGACTAACAGGAAGATGCTTCAAGTTCTCT
GCTCCCTCCTAAAGCTATGCATTAAAGACCATGGGACTTTGCTGGCTTAGAT
CCCTATGGCTATTGCCAGGTTCAATACTATGTATTGCCCTATGCCATATAGTATTCC
ATATATGGGTTTCCTATTGACGTAGATAGCCCCTCCAATGGCGGTCCATATACCA
TATATGGGCTTCCTAATACGCCATAGCCACTCCCCATTGACGTCAATGGTCTCTA
TATATGGTCTTCCTATTGACGTCAATGGCGGTCTATTGACGTATATGGCGCTC
CCCATTGACGTCAATTACGGTAATGGCCCGCTGGCTCAATGCCATTGACGTCAATA
GGACCACCCACCATTGACGTCAATGGGATGGCTATTGCCATTCATATCGTTCTCAC
GCCCTATTGACGTCAATGACGGTAATGGCCCATTGGCAGTACATCAATATCTATT
AATAGTAACGGCAAGTACATTACTATTGAAAGTACGCCAGGGTACATTGGCAGTACT
CCCATTGACGTCAATGGCGGTAAATGGCCCGCGATGGCTGCCAAGTACATCCCCATTGA
CGTCAATGGGAGGGCAATGACGCAAATGGCGTCCATTGACGTAAATGGCGGTAG
GGCGCTTAATGGAGGTCTATATAAGCAATGCTCGTTAGGGAACGCCATTCTGCCT
GGGACGTCGGAGGAGCTGAAAGCTCTAGACAATTGACGCGTAGGCCTGCCCGCG
TCGACCAAGGGCCAGACTGTTAACGGCCTAGGTTAACTCGAGTTGACATCGA
TAATCAACCTCTGGATTACAAAATTGTGAAAGATTGACTGGTATTCTTAACATGTTG
CTCCTTTACGCTATGTGGATACGCTGCTTAATGCCCTTGATCATGCTATTGCTTCC
CGTATGGCTTCATTCTCCTCTGTATAAATCCTGGTGTCTCTTATGAGGA
GTTGGCCCGTTGTCAGGCAACGTGGCGTGTGCACTGTGTTGCTGACGCAACCC
CCACTGGTTGGGCATTGCCACACCTGTCAAGCTCTTCCGGACTTCGCTTCCCC
CTCCCTATTGCCACGGCGGAACTCATGCCGCTGCCATTGCCGCTGGACAGGGC
TCGGCTGTTGGCACTGACAATTCCGTGGTGTGCGGGAAATCATCGCTTCCCTT
GGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCTCTGCTACGTCCCT
TCGGCCCTCAATCCAGCGGACCTCCTCCGCCGCTGCTGCCGGCTGCCGCTCT
TCCGCGTCTCGCCTCGCCCTCAGACGAGTCGGATCTCCCTTGGCCGCTCCCCGC
ATCGATAAAATAAAAGATTGTTATTAGTCTCCAGAAAAAGGGGGAAATGAAAGACCCCA
CCTGTAGGTTGGCAAGCTAGCTTAAGTAACGCCATTGCAAGGCATGGAAAAATACA
TAACTGAGAATAGAGAAGTTCAGATCAAGGTAGGAACAGATGGAACAGCTGAATATGG
GCCAAACAGGATATCTGTTGTAAGCAGTTCTGCCCGCTCAGGGCCAAGAACAGATG
GAACAGCTGAATATGGGCCAACAGGATATCTGTTGTAAGCAGTTCTGCCCGCTCA
GGGCCAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTCTAGAGAACCA

FIGURE 24 (C)

TCAGATGTTCCAGGGTGCCCAAGGACCTGAAATGACCCTGTGCCTTATTGAECTAA
CCAATCAGTCGCTTCTCGCTTCTGTCGCGCTTCTGCTCCCCGAGCTAATAAAG
AGCCCACAACCCCTCACTCGGGCGCCAGTCCTCCGATTGACTGAGTCGCCGGTACCC
CGTGTATCCAATAAACCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCTGG
GAGGGTCTCCTTGAGTGATTGACTACCCGTCAAGCGGGGTCTTCATT 4354

1 - 763	HCMV-MOMUSV CHIMERIC 5'LTR
833 - 1642	EXTENDED PACKAGING REGION
1712 - 2272	MOUSE DHFR GENE CODING REGION
2355 - 3038	SIMIAN CMV PROMOTER
3029 - 3114	MULTIPLE CLONING SITE (SITE OF GENE INSERTION)
3121 - 3721	RESE
3761 - 4354	3'LTR

Figure 25(A)

Glutamine synthase Retrovector gene construct (SEQ ID NO:41)



LTR =	Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat Fusion
Ψ EPR =	Moloney Murine Leukemia Virus Psi Region and Extended Viral Packaging Region
DHFR =	Mouse Glutamine Synthase Gene
CMV =	Simian Cytomegalovirus Promoter Region
MCS =	Multiple Cloning Site (Gene Insertion Site)
RESE =	RNA Export and Stability Element
LTR =	Moloney Murine Leukemia Virus Long Terminal Repeat

1 GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCAATTAGTTCA
ATAGCCCATATATGGAGTTCCCGCGTTACATAACTTACGGTAAATGGCCCGCTGGCTGA
CCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCAGTAGAACGCC
AATAGGGACTTCATTGACGTCAATGGGTGGAGTATTACGGTAAACTGCCACTTGG
CAGTACATCAAGTGTATCATATGCCAAGTACGCCCTATTGACGTCAATGACGGTAAA
TGGCCCGCCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCTACTGGCAGTA
CATCTACGTATTAGTCATCGCTATTACCATGGTATGCAGGTTTGGCAGTACATCAATG
GGCGTGGATAGCGGTTGACTCACGGGATTCCAAGTCTCCACCCATTGACGTCAAT
GGGAGTTGTTGGCACCAAAATCAACGGGACTTCCAAAATGTCGAACAACCTCCGC
CCCATTGACGCAAATGGCGGTAGGCATGTACGGTGGGAGGTCTATAAGCAGAGCTC
AATAAAAGAGCCCACAACCCCTCACTCGCGCGCCAGTCTCCGATAGACTGCGTCGCC
CGGGTACCGTATTCCAATAAGCCTTGTGCTTGCATCCGAATCGTGGCTCGCT
GTTCCCTGGGAGGGTCTCCTCTGAGTGAATGACTACCCACGACGGGGTCTTCATTG
GGGGCTCGTCCGGATTGGAGACCCCTGCCAGGGACCACGACCCACCACCGGGAGG
TAAGCTGGCAGCAACTATCTGTGCTGTCGATTGCTAGTGTCTATGTTGATGTT
ATGCGCCTCGTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGG
AACTGACGAGTTCTGAACACCCGGCGCAACCCCTGGGAGACGTCCAGGGACTTGGGG
GCCGTTTGTGGCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCGTCAAGGA
TATGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTCCCGCTCCGTCTGAATT
GCTTTCGGTTGGAACCGAAGCCCGCGTCTGTGCTGCTGCAGCGCTGCAGCATCGTC
TGTGTTGCTCTGTGACTGTGTTCTGTATTGCTGAAATTAGGGCCAGACTGTT
ACCACTCCCTTAAGTTGACCTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAA
CCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTCTGCTCGCAGAATGGCCAA
CCTTAAACGTGGATGGCCCGAGACGGCACCTTAACCGAGACCTCATCACCCAGGTT
AAGATCAAGGTCTTACCTGGCCCGCATGGACACCCAGACAGGTCCCCTACATCGT

FIGURE 25 (B)

GACCTGGGAAGCCTTGGCTTTGACCCCCCTCCCTGGGTCAAGCCCTTGTACACCTA
AGCCTCCGCCTCCTCTTCCATCCGCCCGTCTCTCCCCCTGAACCTCCTCGTTCG
ACCCCGCCTCGATCCTCCCTTATCCAGCCCTCACTCCTCTCTAGGCCCGAATTCC
GATCTGATCAAGAGACAGGATGAACCCTGGCACCTCAGCAAGTCCCCTGAACAAA
GGCATCAAGCAAATGTACATGTCCCTGCCAGGGTGAGAAAGTCCAAGCCATGTATAT
CTGGGTGATGGTACCGGAGAAGGACTGCCTGCAAGACCCGTACCTGGACTGTGAGC
CCAAGTGTGGAAGAGTTACCTGAGTGGAACTTGTATGGCTCTAGTACCTTCAGTCT
GAAGGCTCCAACAGCGACATGTACCTCCATCCTGTTGCCATGTTGAGACCCCTCCG
CAAAGACCCAACAAGCTGGTCTATGTGAAGTTCAGTATAACCGGAAGCCTGCAG
AGACCAACTTGAGGCACATCTGTAACGGATAATGGACATGGTGAGCAACCAGCACCC
TGGTTGGAATGGAGCAGGAATATACTCTTATGGGAACAGACGGCCACCCATTGGTTG
GCCTTCCAATGGCTTCCCTGGACCCAAGGCCGTATTACTGCCTGTTGAGTC
AGGCCTACGGCAGGGACATCGTGGAGGCTCACTACCGGGCTGCTGTATGCTGGAGTC
AAGATCACGGGACAAATGCGGAGGTTATGCCTGCCAGTGGAAATTCCAGATAGGACC
CTGTGAGGGGATCCGAATGGGAGATCATCTTGGATAGCCGTTTATCTGCATCGG
TGTGCGAAGACTTGGGGTGTAGCAACCTTGACCCCAAGCCCATTCCAGGGAACTGG
AATGGTGCAGGCTGCCATACCAACTTCAGCACCAAGGCCATGCGGGAGGAGATGGTCT
GAAGTGCATTGAGGAGGCCATTGACAAACTGAGCAAGAGGCCAGTACACATCCGCG
CCTACGATCCAAGGGGGCCTGGACAACGCCGGCGTCTGACTGGATTCCACGAAACC
TCCAACATCAACGACTTTCTGCCGTGTTGCCAACGCCGGTGCAGTATCCGATTCC
CCGGACTGTGCCAGGAGAAGAAGGGCTACTTGAGACCGTCCGGCTTCTGCCATT
GTGACCCCTATGCCGTGACAGAACGCCATCGCCACGTCTCCTCAACGAAACAGGC
GACGAACCTTCAATACAAGAACTAAGGATCCCTATGGCTATTGCCAGGTTCAATAC
TATGTATTGCCCTATGCCATATAGTATTCCATATATGGGTTTCTATTGACGTAGAT
AGCCCCCTCCAATGGGGCTCCATATACCATATATGGGCTTCTAATACGCCATA
GCCACTCCCCATTGACGTCAATGGTCTCTATATGGTCTTCTATTGACGTCAATT
GGCGGTCTATTGACGTATGGCGCTCCCCATTGACGTCAATTACGGTAAATGGC
CCGCCTGGCTCAATGCCATTGACGTCAATAGGACCAACCAATTGACGTCAATGGG
TGGCTATTGCCATTCATATCCGTTCTCACGCCCTATTGACGTCAATGACGGTAAA
TGGCCCACTTGGCAGTACATCAATATCTATTAAATAGTAACGGCAAGTACATTACTAT
TGGAAAGTACGCCAGGGTACATTGGCAGTACTCCCATTGACGTCAATGGCGTAAATGGC
CCGCGATGGCTGCCAAGTACATCCCATTGACGTCAATGGGAGGGCAATGACGAAA
TGGCGCTCCATTGACGTAAATGGGCGGTAGGCGTGCCTAATGGGAGGTCTATATAAGC
AATGCTCGTTAGGAACCGCCATTCTGCCGTGGGACGTCGGAGGAGCTGAAAGCTTC
TAGACAATTGACCGTAGGCCTGCCCGCGTCGACCAAGGGCCAGATCTGTTAACCG
GTCCTAGGTTAAACTCGAGTTGACATCGATAATCACCTCTGGATTACAAAATTGT
GAAAGATTGACTGGTATTCTTAACATATGTCCTTACGCTATGTGGATACGCTGC
TTAATGCCCTTGTATCATGCTATTGCTTCCGTATGGCTTTCATTCTCCTCTGT
ATAAAATCCTGGTTGCTGCTCTTATGAGGAGTTGTGGCCCTGTGAGGCAACGTGGC
GTGGTGTGCACTGTGTTGCTGACGCAACCCCCACTGGTGGGCAATTGCCACCGACCTG
TCAGCTCCTTCCGGACTTCGCTTCCCCCTCCATTGCCACGGCGGAACCATCG
CCGCCTGCCATTGCCCGCTGGACAGGGGCTGGCTGTTGGGACTGACAATTCCGTG
GTGTTGTCGGGAAATCATCGTCCTTCCATTGGCTGCTGCCCTGTGTTGCCACCTGGAT

FIGURE 25 (C)

TCTGCGCGGGACGTCCCTCTGCTACGTCCCTCGGCCCTCAATCCAGCGGACCTCCTT
CCCGCGGCCTGCTGCCGGCTCTGCCCTCTCCGCGTCTCGCCTCGCCCTCAGACG
AGTCGGATCTCCCTTGCGCCTCCCCGATCGATAAAATAAAGATTATTTAGT
CTCCAGAAAAAGGGGGAAATGAAAGACCCCACCTGAGTTGGCAAGCTAGCTTAAGT
AACGCCATTTGCAAGGCATGGAAAATACATAACTGAGAATAGAGAAGTCAGATCAA
GGTCAGGAACAGATGGAACAGCTGAATATGGGCAAACAGGATATCTGTGGTAAGCAGT
TCCTGCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCAAACAGGAT
ATCTGTGGTAAGCAGTCCCTGCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGC
GGTCCAGCCCTCAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGCCCAAGGAC
CTGAAATGACCTGTGCCTATTGAACTAACCAATCAGTCGCTCTCGCTCTGTT
GCGCGCTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTGGGGCGCCA
GTCCTCGATTGACTGAGTCGCCGGTACCCGTATCCAATAACCCCTCTGCAGTT
GCATCCGACTTGTGGTCTGCTGTTCTGGGAGGGTCTCCTCTGAGTGATTGACTACC
CGTCAGCGGGGTCTTCATT 4797

1 - 763	HCMV-MOMUSV CHIMERIC 5'LTR
833 - 1642	EXTENDED PACKAGING REGION
1677 - 2795	MOUSE GLUTAMINE SYNTHASE GENE CODING REGION
2805 - 3472	SIMIAN CMV PROMOTER
3473 - 3558	MULTIPLE CLONING SITE (SITE OF GENE INSERTION)
3565 - 4165	RESE
4205 - 4797	3'LTR